

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:39:31 ; Search time 158 Seconds

(without alignments)
862.767 Million cell updates/sec

Title: US-10-676-358-1

Perfect score: 2085

Sequence: 1 EHFPPKYLHYDETSHTQLLC.....QKLFLEWIGNQVQSVKISCL 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_23Sep04.*

1: geneseqp1980s.*

2: geneseqp1930s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2085	100.0	380	4 AAB66988	Murine OP
2	2085	100.0	380	8 ADM28827	Human ost
3	2085	100.0	381	8 ADM28870	Human OP
4	2085	100.0	382	8 ADM28869	Human OP
5	2085	100.0	385	8 ADM28876	Human OP
6	2085	100.0	391	8 ADM28877	Human OP
7	2085	100.0	400	6 ABU08820	Human ost
8	2085	100.0	401	2 AAW38345	Human ost
9	2085	100.0	401	3 AAY43400	Osteoprot
10	2085	100.0	401	4 AAB66976	Human OP
11	2085	100.0	401	5 ABG71823	Wild type
12	2085	100.0	401	6 ABP55109	Human ost
13	2085	100.0	401	6 AAE34363	Human ost
14	2085	100.0	401	7 AD01627	Human ost
15	2085	100.0	401	8 ADM28813	Human ost
16	2085	100.0	537	6 AAC19639	Human mil
17	2080	99.8	401	5 ABG73895	Human OP
18	2080	99.8	401	5 ABG73894	Human OP
19	2079	99.7	380	2 AAR99924	Mature os
20	2079	99.7	380	6 AAC19638	Human mil
21	2079	99.7	380	7 ADF15245	Human alb
22	2079	99.7	380	8 ADM28860	Human ost
23	2079	99.7	391	2 AAW53238	Human OCI
24	2079	99.7	401	2 AAR99925	Full leng
25	2079	99.7	401	2 AAW53239	Human OCI

26	2079	99.7	401	2 AAY05742	Tumour ne
27	2079	99.7	401	2 AAW95030	Tumour ne
28	2079	99.7	401	2 AAW83926	Human FTH
29	2079	99.7	401	3 AAY88622	Osteoclas
30	2079	99.7	401	3 AAB18715	A human t
31	2079	99.7	401	4 AAB60570	Human TNF
32	2079	99.7	401	5 ABG73893	Human OP
33	2079	99.7	401	6 AAE36245	Human TRA
34	2079	99.7	401	6 AAO31135	Human TRA
35	2079	99.7	401	6 ABP70997	Human ost
36	2079	99.7	401	7 ADD01625	Human ost
37	2079	99.7	401	7 ADD37427	Human ost
38	2079	99.7	401	7 ADF16158	Human alb
39	2079	99.7	401	7 ADF16153	Human alb
40	2079	99.7	401	7 ADF16151	Human alb
41	2079	99.7	401	7 ADF15231	Human alb
42	2079	99.7	401	7 ADF16152	Human alb
43	2079	99.7	401	7 ADF16154	Human alb
44	2079	99.7	401	7 ADF16155	Human alb
45	2079	99.7	401	7 ADF16156	Human alb

ALIGNMENTS

RESULT 1

AAB66988
ID AAB66988 standard; protein; 380 AA.

XX AAB66988;

XX 19-APR-2001 (first entry)

XX Murine OPG cysteine-rich domain.

XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
systemic lupus erythematosus; graft-versus-host disease; septic shock;
acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
ischaemia; Parkinson's disease.

XX Mus sp.

XX WO200103719-A2.

XX 18-JAN-2001.

XX 07-JUL-2000; 2000WO-US018667.

XX 09-JUL-1999; 99US-00350670.

XX 09-DEC-1999; 99US-00457647.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

XX WPI; 2001-103031/11.

XX Treating conditions leading to bone loss such as rheumatoid arthritis,
multiple sclerosis and asthma, comprises administering an osteoprotegerin
protein in conjunction with e.g. inhibitors of interleukin and tumor
necrosis factor alpha.

XX Disclosure; Fig 12; 316pp; English.

XX The present invention relates to a method for treating conditions leading
to bone loss. The method comprises administering a purified and isolated
osteoprotegerin (OPG) protein (AA057836-AA057838 and AAB66974-AAB66976)
in conjunction with other substances such as tumour necrosis factor-alpha
(TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, IGF
modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet

activating factor (PAP) antagonists. The method is useful for treating conditions leading to bone loss such as rheumatoid arthritis, multiple sclerosis, osteoporosis, osteomyelitis and asthma. The method is also useful for treating inflammation, systemic lupus erythematosus (SLE) and graft-versus-host disease (GVHD). Other diseases that can be treated include acute pancreatitis, Alzheimer's disease, anorexia, atherosclerosis, coronary conditions (e.g. myocardial infarction), cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia, inflammatory bowel disease, ischaemia, pain, Parkinson's disease, psoriasis and septic shock

Sequence 380 AA;

Query Match 100.0%; Score 2085; DB 4; Length 380;
Best Local Similarity 100.0%; Pred. No. 5.2e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCTAKWKVVCAPDPHYTDSWHTSDECL 60
Db 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCTAKWKVVCAPDPHYTDSWHTSDECL 60
QY 61 YCSPVCKELQYVKECNTHNRVCECKGRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120
Db 61 YCSPVCKELQYVKECNTHNRVCECKGRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120
QY 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CGNSSESTOKCGIDVTL 180
Db 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CGNSSESTOKCGIDVTL 180
QY 181 CEAEAFRAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKROHSQEQTFQLLKLWKHON 240
Db 181 CEAEAFRAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKROHSQEQTFQLLKLWKHON 240
QY 241 KAQDIVKLLIQLDIDICENSQVORHIGHANLTFEQLSLMESLPKKGVAEDIEKTKACKP 300
Db 241 KAQDIVKLLIQLDIDICENSQVORHIGHANLTFEQLSLMESLPKKGVAEDIEKTKACKP 300
QY 301 SQIILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKKTIRFLRSFTWKLY 360
Db 301 SQIILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKKTIRFLRSFTWKLY 360
QY 361 QKLFLEMGNOVQSVKISCL 380
Db 361 QKLFLEMGNOVQSVKISCL 380

RESULT 2

ADM28827

ID ADM28827 standard; protein; 380 AA.

XX ADM28827;

AC ADM28827;

DT 20-MAY-2004 (first entry)

XX Human osteoprotegerin cysteine-rich domains 1-4 plus C-terminus #1.

XX Mouse; OPG; bone resorption; excessive bone loss; osteoporosis;
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
KW Riley-day syndrome; immobilisation of extremity; tumour;
KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
KW osteoprotegerin; transgenic.

XX Mus sp.

XX US2003207827-A1.

XX 06-NOV-2003.

XX 24-SEP-1999; 99US-00405032.

XX

PR 22-DEC-1995; 95US-005777788.

PR 03-SEP-1996; 96US-00706945.

PR 20-DEC-1996; 96US-00771777.

PR 12-AUG-1998; 98US-00132985.

XX (BOYLE/) BOYLE W J.

PA (LACEY/) LACEY D L.

PA (CALZ/) CALZONE F J.

PA (CHAN/) CHANG M.

XX

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;

XX WPI; 2004-041572/04.

XX Novel osteoprotegerin useful for treating conditions resulting in bone

PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone

PT loss caused by rheumatoid arthritis or osteomyelitis.

XX

PS Disclosure; SEQ ID NO 139; 141pp; English.

XX

CC The invention relates to a purified and isolated polypeptide having
CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
CC having amino terminus at residue 22, and 1-216 amino acids are deleted
CC from carboxy terminus of human OPG polypeptide. Also included are an
CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
CC vector comprising OPG NA, a host cell transformed or transfected with the
CC vector, a transgenic mammal comprising the cell, producing OPG, a
CC polypeptide comprising an amino acid sequence of at least about 164 amino
CC acids comprising four cysteine-rich domains characteristic of the
CC cysteine rich domains of tumour necrosis factor receptor extracellular
CC regions (and an activity of increasing bone density), an antibody (Ab) or
CC its fragment which specifically binds to OPG, a composition comprising
CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
CC Ab is useful for detecting the presence of OPG in a biological sample
CC which involves incubating the sample with Ab under conditions that allow
CC binding of ab to OPG and detecting the bound Ab. OPG is useful for
CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
CC useful for regulating the levels of OPG in an animal (human). The nucleic
CC acid promotes an increasing in tissue level of OPG. OPG is useful for
CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
CC method further involves administering a substance chosen from bone
CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
CC parathyroid hormone related protein and their analogues, E series of
CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
CC useful for treating osteoporosis such as primary osteoporosis, endocrine
CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
CC osteoporosis due to immobilisation of extremities, hypercalcaemia
CC resulting from solid tumours and haematologic malignancies (multiple
CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
CC hypercalcaemia associated with hyperthyroidism and renal function
CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
CC death. The present sequences is an OPG protein (or fragment).

XX

SQ Sequence 380 AA;

Query Match 100.0%; Score 2085; DB 8; Length 380;

Best Local Similarity 100.0%; Pred. No. 5.2e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCTAKWKVVCAPDPHYTDSWHTSDECL 60

Db 1 ETFFPKYLHYDEETSHQLLCKCPGGTYLKQCTAKWKVVCAPDPHYTDSWHTSDECL 60

QY 61 YCSPVCKELQYVKECNTHNRVCECKGRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120

Db 61 YCSPVCKELQYVKECNTHNRVCECKGRYLEIFCLKHSRCPGFGVVQAGTPERNTV 120

QY 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CGNSSESTOKCGIDVTL 180

Db 121 CKRCPDGFPSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CGNSSESTOKCGIDVTL 180

QY 181 CEAEAFRAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKROHSQEQTFQLLKLWKHON 240

Db 181 CEAEAFRAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKROHSQEQTFQLLKLWKHON 240

QY 241 KAQDIVKLLIQLDIDICENSQVORHIGHANLTFEQLSLMESLPKKGVAEDIEKTKACKP 300

Db 241 KAQDIVKLLIQLDIDICENSQVORHIGHANLTFEQLSLMESLPKKGVAEDIEKTKACKP 300

QY 301 SQIILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKKTIRFLRSFTWKLY 360

Db 301 SQIILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKKTIRFLRSFTWKLY 360

QY 361 QKLFLEMGNOVQSVKISCL 380

Db 361 QKLFLEMGNOVQSVKISCL 380

Db 61 YCSPVCKELQYVQKQCNRTHNRVCECKEGRYLEIEFCLKHSRCPGGVVOAGTPERNTV 120
 QY 121 CKRCPDGFSSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTL 180
 Db 121 CKRCPDGFSSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTL 180
 QY 181 CEEAFRFAVPTKFTPNWLSVLDNLPCTKNAESVERIKRQHSOBQTFOLLKLWKHQ 240
 Db 181 CEEAFRFAVPTKFTPNWLSVLDNLPCTKNAESVERIKRQHSOBQTFOLLKLWKHQ 240
 QY 241 KAQDIVKKIQQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
 Db 241 KAQDIVKKIQQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
 QY 301 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKTIKIRFLHSFTMYKLY 360
 Db 301 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKTIKIRFLHSFTMYKLY 360
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 361 QKLFLEMIGNQVQSVKISCL 380
 RESULT 3
 ADM28870
 ID ADM28870 standard; protein; 381 AA.
 XX
 AC ADM28870;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human OPG truncation mutant, OPG met[22-401].
 XX
 KW Human; OPG; bone resorption; excessive bone loss; osteoporosis;
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
 KW Riley-day syndrome; immobilisation of extremity; tumour;
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
 KW osteoprotegerin; transgenic; mutant; mutein.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN US2003207827-A1.
 XX
 PD 06-NOV-2003.
 XX
 PF 24-SEP-1999; 99US-00405032.
 XX
 PR 22-DEC-1995; 95US-00577788.
 PR 03-SEP-1996; 96US-00706945.
 PR 20-DEC-1996; 96US-00717177.
 PR 12-AUG-1998; 98US-00132985.
 XX
 PA (BOYL/) BOYLE W J.
 PA (LACE/) LACEY D L.
 PA (CALZ/) CALZONE F J.
 PA (CHAN/) CHANG M.
 XX
 FI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
 XX WPI; 2004-041572/04.
 XX
 PT Novel osteoprotegerin useful for treating conditions resulting in bone
 PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
 PT loss caused by rheumatoid arthritis or osteomyelitis.
 XX
 PS Claim 37; Page; 141pp; English.
 XX
 CC The invention relates to a purified and isolated polypeptide having

CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
 CC having amino terminus at residue 22, and 1-216 amino acids are deleted
 CC from carboxy terminus of human OPG polypeptide. Also included are an
 CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
 CC vector comprising OPG NA, a host cell transformed or transfected with the
 CC vector, a transgenic mammal comprising the cell, producing OPG, a
 CC polypeptide comprising an amino acid sequence of at least about 164 amino
 CC acids comprising four cysteine-rich domains characteristic of the
 CC cysteine rich domains of tumour necrosis factor receptor extracellular
 CC regions (and an activity of increasing bone density), an antibody (Ab) or
 CC its fragment which specifically binds to OPG, a composition comprising
 CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
 CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
 CC Ab is useful for detecting the presence of OPG in a biological sample
 CC which involves incubating the sample with Ab under conditions that allow
 CC binding of Ab to OPG and detecting the bound Ab. OPG is useful for
 CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
 CC useful for regulating the levels of OPG in an animal (human). The nucleic
 CC acid promotes an increasing in tissue level of OPG. OPG is useful for
 CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
 CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
 CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
 CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
 CC method further involves administering a substance chosen from bone
 CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
 CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
 CC parathyroid hormone related protein and their analogues. E series of
 CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
 CC useful for treating osteoporosis such as primary osteoporosis, endocrine
 CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
 CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
 CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
 CC osteoporosis due to immobilisation of extremities, hypercalcaemia
 CC resulting from solid tumours and haematologic malignancies (multiple
 CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
 CC hypercalcaemia associated with hyperthyroidism and renal function
 CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
 CC death. The present sequences is an OPG truncation/deletion or
 CC substitution mutant protein (or fragment).
 XX
 SQ Sequence 381 AA;

Query Match 100.0%; Score 2085; DB 8; Length 381;
 Best Local Similarity 100.0%; Pred. No. 5.2e-153;
 Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ETTPPKYLHYDEETSHQLLCDKCPGGYLLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 60
 Db 2 ETTPPKYLHYDEETSHQLLCDKCPGGYLLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 61
 QY 61 YCSPVCKELQVVKQCNRTHNRVCECKEGRYLEIEFCLKHSRCPGGVVOAGTPERNTV 120
 Db 62 YCSPVCKELQVVKQCNRTHNRVCECKEGRYLEIEFCLKHSRCPGGVVOAGTPERNTV 121
 QY 121 CKRCPDGFSSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTL 180
 Db 122 CKRCPDGFSSNETSSKAPCKKHTNCSVFGLLLTQKGNATHDNI CSNSESSTQKCGIDVTL 181
 QY 181 CEEAFRFAVPTKFTPNWLSVLDNLPCTKNAESVERIKRQHSOBQTFOLLKLWKHQ 240
 Db 182 CEEAFRFAVPTKFTPNWLSVLDNLPCTKNAESVERIKRQHSOBQTFOLLKLWKHQ 241
 QY 241 KAQDIVKKIQQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
 Db 242 KAQDIVKKIQQIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 301
 QY 301 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKTIKIRFLHSFTMYKLY 360
 Db 302 SDQILKLLSLWRINKGQDQTLKGLMHALKSKTYHFPKTVTQSLKTIKIRFLHSFTMYKLY 361
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 362 QKLFLEMIGNQVQSVKISCL 381

RESULT 4
ADM28869
ID ADM28869 standard; protein; 382 AA.
XX
AC ADM28869;
XX
DT 20-MAY-2004 (first entry)
XX
DE Human OPG truncation mutant, OPG met-lys[22-401].
XX
KW Human; OPG; bone resorption; excessive bone loss; osteoporosis;
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
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KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
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KW Riley-day syndrome; immobilisation of extremity; tumour;
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KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
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XX
OS Homo sapiens.
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XX
FN US2003207827-A1.
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PD 06-NOV-2003.
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PR 12-AUG-1998; 98US-00132985.
XX
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XX
PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
XX
DR WPI; 2004-041572/04.
XX
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CC acids comprising four cysteine-rich domains characteristic of the
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CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
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CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced

CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
CC method further involves administering a substance chosen from bone
CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
CC parathyroid hormone related protein and their analogues, E series of
CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
CC useful for treating osteoporosis such as primary osteoporosis, endocrine
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CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
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CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
CC hypercalcaemia associated with hyperthyroidism and renal function
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CC death. The present sequences is an OPG truncation/deletion or
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Query Match 100.0%; Score 2085; DB 8; Length 382;
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QY 1 ETFPPKYLHYDETSQQLLCKCPGTYLKQCTAKWTKVACPDHYVYDTSWHTSDECL 60
DB 3 ETFPPKYLHYDETSQQLLCKCPGTYLKQCTAKWTKVACPDHYVYDTSWHTSDECL 62
QY 61 YCSPVCKELQYVYQECNRTNHRVCEKGRYLEIEFCLKHSRCPFGVGVQAGTPERTV 120
DB 63 YCSPVCKELQYVYQECNRTNHRVCEKGRYLEIEFCLKHSRCPFGVGVQAGTPERTV 122
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSESTOKCGIDVTL 180
DB 123 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSESTOKCGIDVTL 182
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRHSQBQTFOLLKWKHON 240
DB 183 CEEAFFRFAVPTKFTPNWLSVLVDNLPQTKVNAESVERIKRHSQBQTFOLLKWKHON 242
QY 241 KAQDIVVKIIQDILCENSQVRHGHANLTFEQLRSLMESLFGKVGAGEDIKTIKACP 300
DB 243 KAQDIVVKIIQDILCENSQVRHGHANLTFEQLRSLMESLFGKVGAGEDIKTIKACP 302
QY 301 SDQILKLSLWRIKNGDQDTLKGLMHALKSKTYHFKPTVTSQSLKKTIRFLHSFTMYKLY 360
DB 303 SDQILKLSLWRIKNGDQDTLKGLMHALKSKTYHFKPTVTSQSLKKTIRFLHSFTMYKLY 362
QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 363 QKLFLEMIGNOVQSVKISCL 382

RESULT 5
ADM28876
ID ADM28876 standard; protein; 385 AA.

XX ADM28876;
XX

DT 20-MAY-2004 (first entry)

XX Human OPG truncation mutant, OPG met-met-(lys)3[22-401].

XX Human; OPG; bone resorption; excessive bone loss; osteoporosis;
KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
KW Riley-day syndrome; immobilisation of extremity; tumour;
KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
KW osteoprotegerin; transgenic; mutant; mutein.

XX WPI; 2004-041572/04.
XX Novel osteoprotegerin useful for treating conditions resulting in bone
XX loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
XX loss caused by rheumatoid arthritis or osteomyelitis.
XX
XX Claim 37; Page; 141pp; English.
XX
XX The invention relates to a purified and isolated polypeptide having
XX osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
XX having amino terminus at residue 22, and 1-216 amino acids are deleted
XX from carboxy terminus of human OPG polypeptide. Also included are an
XX isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
XX vector comprising OPG NA, a host cell transformed or transfected with the
XX vector, a transgenic mammal comprising the cell, producing OPG, a
XX polypeptide comprising an amino acid sequence of at least about 164 amino
XX acids comprising four cysteine-rich domains characteristic of the
XX cysteine rich domains of tumour necrosis factor receptor extracellular
XX regions (and an activity of increasing bone density), an antibody (Ab) or
XX its fragment which specifically binds to OPG, a composition comprising
XX OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
XX and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
XX Ab is useful for detecting the presence of OPG in a biological sample
XX which involves incubating the sample with Ab under conditions that allow
XX binding of Ab to OPG and detecting the bound Ab. OPG is useful for
XX assessing the ability of a candidate substance to bind to OPG. OPG NA is
XX useful for regulating the levels of OPG in an animal (human). The nucleic
XX acid promotes an increasing in tissue level of OPG. OPG is useful for
XX treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
XX disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
XX osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
XX osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
XX method further involves administering a substance chosen from bone
XX morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
XX inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
XX parathyroid hormone related protein and their analogues, E series of
XX prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
XX useful for treating osteoporosis such as primary osteoporosis, endocrine
XX osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
XX hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
XX, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
XX osteoporosis due to immobilisation of extremities, hypercalcaemia
XX resulting from solid tumours and haematologic malignancies (multiple
XX myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
XX hypercalcaemia associated with hyperthyroidism and renal function
XX disorders, osteopaenia following surgery and osteonecrosis or bone cell
XX death. The present sequences is an OPG truncation/deletion or
XX substitution mutant protein (or fragment).

XX Sequence 391 AA;
XX
XX Query Match 100.0%; Score 2085; DB 8; Length 391;
XX Best Local Similarity 100.0%; Pred. No. 5.3e-153;
XX Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 BTFPPKYLHYDETSQHLCDKCPGGTYLKQHTAKWTKVACPDHYTDSWHTSDECL 60
XX 12 BTFPPKYLHYDETSQHLCDKCPGGTYLKQHTAKWTKVACPDHYTDSWHTSDECL 71
XX
XX 61 YCSVPCKELQVVKQECNTHNRVCECKGRYLETFCLKHRSCTPPGFGVQAGTPERNTV 120
XX 72 YCSVPCKELQVVKQECNTHNRVCECKGRYLETFCLKHRSCTPPGFGVQAGTPERNTV 131
XX
XX 121 CKRPDGFSSNETSSKAPCRHTNCSVFGILLTQKGNATHDNI CSGNSESTQKCGIDVTLL 180
XX 132 CKRPDGFSSNETSSKAPCRHTNCSVFGILLTQKGNATHDNI CSGNSESTQKCGIDVTLL 191
XX
XX 181 CEEAFFRFAVPTKFTPNMLSVLNDLPCTKVNAESVERIKQHSSEQEOTFOLLKWKHQN 240
XX 192 CEEAFFRFAVPTKFTPNMLSVLNDLPCTKVNAESVERIKQHSSEQEOTFOLLKWKHQN 251
XX
XX 241 KQADIVKKIIQDIDLCENSQVRHIGHANLTFQLRSLMESLPGKKVGAEDIEKTIKACP 300

XX Db 252 KQADIVKKIIQDIDLCENSQVRHIGHANLTFQLRSLMESLPGKKVGAEDIEKTIKACP 311
XX QY 301 SQOILKLSLWPKIKNGDQDTLKGIMHALKSKTYHFPKTVTQSLKKTIRPLHSFTMYKLY 360
XX Db 312 SQOILKLSLWPKIKNGDQDTLKGIMHALKSKTYHFPKTVTQSLKKTIRPLHSFTMYKLY 371
XX
XX QY 361 QKLFLFLEMIGNQVQSVKISCL 380
XX Db 372 QKLFLFLEMIGNQVQSVKISCL 391
XX
XX RESULT 7
XX ABU08820
XX ID ABU08820 standard; protein; 400 AA.
XX AC ABU08820;
XX DT 13-AUG-2003 (first entry)
XX DE Human osteoprotegerin protein.
XX KW Human; osteoprotegerin; endothelial morphogenesis; capillary formation.
XX OS Homo sapiens.
XX PN US2003022834-A1.
XX PD 30-JAN-2003.
XX PF 09-MAY-2002; 2002US-00142658.
XX PR 10-MAY-2001; 2001US-0290230P.
XX PA (MALY/) MALYANKAR U M.
XX PA (SCAT/) SCATENA M.
XX PA (GIAC/) GIACHELLI C M.
XX PI Malyankar UM, Scatena M, Giachelli CM;
XX WPI: 2003-479494/45.
XX DR N-PSDB; ABX93089.
XX
XX Promoting endothelial morphogenesis for promoting formation of blood
XX vessels, e.g. capillaries, in vivo in an area of damaged mammalian heart
XX muscle, involves providing osteoprotegerin to one or more endothelial
XX cells.
XX
XX Claim 3; Page 9-10; 15pp; English.
XX
XX This invention relates to a novel method for promoting endothelial
XX morphogenesis, comprises providing osteoprotegerin to one or more
XX endothelial cells. The invention also discloses an implantable medical
XX device comprising a device body and a layer attached to a surface of the
XX device body. The layer comprises a molecule such as osteoprotegerin or a
XX nucleic acid molecule encoding osteoprotegerin, where the device is
XX adapted to be completely or partially implanted into an animal body. The
XX method of the invention is useful for promoting in vivo endothelial
XX morphogenesis, such as the formation of capillaries which are formed in
XX tissue (e.g. heart tissue) adjacent to an implanted medical device or the
XX formation of an endothelial lining in a blood vessel, an artificial or
XX natural blood vessel. The method is also useful for promoting endothelial
XX morphogenesis in vitro. The implanted medical device is useful for
XX promoting endothelial morphogenesis in any situation, e.g. promotion of
XX blood vessel growth in and around damaged heart muscle. The implanted
XX medical device promotes the growth of blood vessels in the surrounding
XX tissue, thereby reducing or preventing the formation of a collagenous
XX capsule around the implanted medical device and foreign body reaction.
XX The method is useful for promoting formation of blood vessels in vivo
XX such as in an area of mammalian heart muscle that has been damaged, such
XX as by reduced blood flow resulting from heart attack. The present
XX sequence represents the human Osteoprotegerin protein which is used in
XX the method of the invention to promote endothelial morphogenesis

```

XX      Sequence 400 AA;
SQ
Query Match      100.0%; Score 2085; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ETTPPKYLHYDEBTSHQLLDCDCPPGTYLKQHCTAKWTVCAFCPDHYTDSWHTSDECL 60
DB      21  ETTPPKYLHYDEBTSHQLLDCDCPPGTYLKQHCTAKWTVCAFCPDHYTDSWHTSDECL 80

QY      61  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVOAGTPPENTV 120
DB      81  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVOAGTPPENTV 140

QY      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
DB      141  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 200

QY      181  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKRQSSOBTQFLLKLWKHQN 240
DB      201  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKRQSSOBTQFLLKLWKHQN 260

QY      241  KAQDIVKKIIQIDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
DB      261  KAQDIVKKIIQIDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 320

QY      301  SDQILKLLSLWRINKGDDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB      321  SDQILKLLSLWRINKGDDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 380

QY      361  QKLFLEMIGNQVQSVKISCL 380
DB      381  QKLFLEMIGNQVQSVKISCL 400

RESULT 8
AAW38345
ID      AAW38345 standard; protein; 401 AA.
XX
AC      AAW38345;
XX
DT      20-APR-1998 (first entry)
XX
DE      Human osteoprotegerin.
XX
KW      Osteoprotegerin; antibody; diagnosis; affinity purification;
KW      recombinant production; transgenic animal; treatment; prevention;
KW      antisense oligonucleotide; probe; detection; screening; human;
KW      bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW      hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW      osteolytic metastasis; periodontal bone loss; bone necrosis; osteopaenia.
XX
OS      Homo sapiens.
XX
PN      D819654610-A1.
XX
PD      26-JUN-1997.
XX
PF      20-DEC-1996; 96DE-01054610.
XX
PR      22-DEC-1995; 95US-00577788.
PR      03-SEP-1996; 96US-00706945.
XX
PA      (AMGE-) AMGEN INC.
XX
PI      Boyle WJ, Lacey DL, Calzone FJ, Chang M;
XX
DR      WPI; 1997-334271/31.
XX
DR      N-PSDE; AAT96063.
XX
PT      Nucleic acid encoding osteoprotegerin - useful for treatment of diseases
PT      involving excessive bone loss, e.g. osteoporosis.

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XX      Claim 23; Page 109-111; 182pp; German.
XX
CC      The present sequence is human osteoprotegerin (OPG). Anti-OPG antibodies
CC      can be used in OPG diagnostic assays, and as affinity purification
CC      materials. The OPG cDNA can be used to express recombinant OPG and to
CC      generate transgenic animals. It can also be used to regulate the level of
CC      OPG in mammals, specifically to increase OPG levels, however the use of
CC      antisense sequences is also contemplated. Fragments of the cDNA can be
CC      used as probes to detect OPG expressing cells and tissue, and to screen
CC      cDNA libraries for related sequences. OPG can be used to treat or prevent
CC      bone diseases, specifically excessive bone loss, e.g. osteoporosis,
CC      Paget's disease, hypercalcaemia, hyperparathyroidism, rheumatoid
CC      arthritis, osteomyelitis, osteolytic metastases, periodontal bone loss,
CC      bone necrosis and osteopaenia
XX
SQ      Sequence 401 AA;
Query Match      100.0%; Score 2085; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  ETTPPKYLHYDEBTSHQLLDCDCPPGTYLKQHCTAKWTVCAFCPDHYTDSWHTSDECL 60
DB      22  ETTPPKYLHYDEBTSHQLLDCDCPPGTYLKQHCTAKWTVCAFCPDHYTDSWHTSDECL 81

QY      61  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVOAGTPPENTV 120
DB      82  YCSPVCKELQYVQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVVOAGTPPENTV 141

QY      121  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 180
DB      142  CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCSGNSESTQKCGIDVTL 201

QY      181  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKRQSSOBTQFLLKLWKHQN 240
DB      202  CEEAFRFAVPTFTPNWLSVLDNLPGTKVNAESVERIKRQSSOBTQFLLKLWKHQN 261

QY      241  KAQDIVKKIIQIDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 300
DB      262  KAQDIVKKIIQIDILCENSQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP 321

QY      301  SDQILKLLSLWRINKGDDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB      322  SDQILKLLSLWRINKGDDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY      361  QKLFLEMIGNQVQSVKISCL 380
DB      382  QKLFLEMIGNQVQSVKISCL 401

RESULT 9
AAW43400
ID      AAW43400 standard; protein; 401 AA.
XX
AC      AAW43400;
XX
DT      28-JAN-2000 (first entry)
XX
DE      Osteoprotegerin protein sequence.
XX
KW      Osteoprotegerin; OPG; human; cardiovascular disease; occlusion;
KW      calcification; blood vessel; atherosclerosis; medial calcific sclerosis;
KW      Monckeberg's arteriosclerosis; therapy.
XX
OS      Homo sapiens.
XX
PN      WO9953942-A1.
XX
PD      28-OCT-1999.
XX
PF      21-APR-1999; 99WO-US008793.
XX

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PR 23-APR-1998; 98US-00064832.
XX (AMGE-) AMGEN INC.
XX Simonet S, Sarosi I;
XX WPI; 2000-013182/01.
XX DR N-PSDB; AA237254.
XX
PT Treating and preventing cardiovascular diseases, especially
XX atherosclerosis and Monckeberg's arteriosclerosis.
XX
PS Claim 9; Page 37-39; 43pp; English.
XX
CC This sequence represents the human osteoprotegerin (OPG). The invention
XX relates to a method of treating or preventing cardiovascular disease by
XX administering OPG. The method can be used to treat and prevent
XX cardiovascular diseases associated with occlusion and calcification of
XX blood vessels, especially atherosclerosis or Monckeberg's
XX arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or
XX prevent cardiovascular diseases provides an alternative to invasive
XX treatments. OPG can be used as a single therapeutic for prevention and
XX treatment of both osteoporosis and cardiovascular diseases
XX
XX Sequence 401 AA;
SQ
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETPPKYLHYDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCDPDHYTDSWHTSDCL 60
DB 22 ETPPKYLHYDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCDPDHYTDSWHTSDCL 81
QY 61 YCSPVKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPFGVQAGTPERNTV 120
DB 82 YCSPVKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPFGVQAGTPERNTV 141
QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 180
DB 142 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKNAESVERIKRQHSQEQTFOLLKWKQN 240
DB 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKNAESVERIKRQHSQEQTFOLLKWKQN 261
QY 241 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACP 300
DB 262 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACP 321
QY 301 SDQILKLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNOVSVKISCL 380
DB 382 QKLFLEMIGNOVSVKISCL 401
RESULT 10
AAB66976
ID AAB66976 standard; protein; 401 AA.
XX
XX AAB66976;
AC
XX
DT 19-APR-2001 (first entry)
XX
DE Human OPG.
XX
KW Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;

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KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW endometriosis; fever; glomerulonephritis; inflammatory bowel disease;
XX ischaemia; Parkinson's disease.
XX Homo sapiens.
XX WO200103719-A2.
XX 18-JAN-2001.
XX
XX 07-JUL-2000; 2000WO-US018667.
XX
XX 09-JUL-1999; 99US-00350670.
XX 09-DEC-1999; 99US-00457647.
XX (AMGE-) AMGEN INC.
XX
XX Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;
XX WPI; 2001-103031/11.
XX DR N-PSDB; AAF57838.
XX
XX Treating conditions leading to bone loss such as rheumatoid arthritis,
XX multiple sclerosis and asthma, comprises administering an osteoprotegerin
XX protein in conjunction with e.g. inhibitors of interleukin and tumor
XX necrosis factor alpha.
XX
XX Example 5; Fig 9; 316pp; English.
XX
XX The present invention relates to a method for treating conditions leading
XX to bone loss. The method comprises administering a purified and isolated
XX osteoprotegerin (OPG) protein (AAF57836-AAF57838 and AAB66974-AAB66976)
XX in conjunction with other substances such as tumour necrosis factor-alpha
XX (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, IGF
XX modulators, fibroblast growth factor (FGF) 1-10 modulators and/or platelet
XX activating factor (PAF) antagonists. The method is useful for treating
XX conditions leading to bone loss such as rheumatoid arthritis, multiple
XX sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
XX useful for treating inflammation, systemic lupus erythematosus (SLE) and
XX graft-versus-host disease (GVHD). Other diseases that can be treated
XX include acute pancreatitis, Alzheimer's disease, anorexia,
XX atherosclerosis, coronary conditions (e.g. myocardial infarction),
XX cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,
XX inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
XX psoriasis and septic shock
XX
XX Sequence 401 AA;
SQ
Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETPPKYLHYDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCDPDHYTDSWHTSDCL 60
DB 22 ETPPKYLHYDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCDPDHYTDSWHTSDCL 81
QY 61 YCSPVKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPFGVQAGTPERNTV 120
DB 82 YCSPVKELQVVKQECNTHNRVCEKGRYLEIEFCLKHSRCPFGVQAGTPERNTV 141
QY 121 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 180
DB 142 CKRCPDGFSSNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVT 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKNAESVERIKRQHSQEQTFOLLKWKQN 240
DB 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKNAESVERIKRQHSQEQTFOLLKWKQN 261
QY 241 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACP 300
DB 262 KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRSLMESLP GKKGVAEDIEKTIKACP 321
QY 301 SDQILKLSLWRKINGDQDTLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360

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Db 322 SDQILKLLSLWRIKNGDQTLKGLMHALKHSTKYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
361 QKLFLEMIGNQVQSVKISL 380
382 QKLFLEMIGNQVQSVKISL 401
RESULT 11
ABG71823
ID ABG71823 standard; protein; 401 AA.
AC ABG71823;
XX
DT 14-APR-2003 (first entry)
XX
DE Wild type human OPG (osteoprotegerin) protein.
XX
KW RANKL; human receptor activator of Nf-kappaB; osteoprotegerin; OPG;
KW RANK ligand; osteoclastogenesis; osteoclast inhibitor; gene therapy;
KW osteoporosis; bone disease; human.
XX
OS Homo sapiens.
XX WO200264782-A2.
XX
XX 22-AUG-2002.
XX
XX 08-FEB-2002; 2002WO-DK000090.
XX
XX 09-FEB-2001; 2001DK-00000214.
PR 09-FEB-2001; 2001US-0267843P.
PR 23-MAR-2001; 2001DK-00000498.
PR 23-MAR-2001; 2001US-0278320P.
XX
XX (MAXY-) MAXYGEN HOLDINGS LTD.
XX
XX Haaning JM, Halkier T;
XX WPI; 2002-691592/74.
XX
XX Novel human receptor activator of Nf-kappaB (hRANK) or human
PT osteoprotegerin (hOPG) variant polypeptides which bind to RANK ligand
PT (RANKL) with equivalent binding affinity as hRANK or hOPG, useful for
PT treating osteoporosis.
XX
XX Example 6; Fig 2; 129pp; English.
XX
XX This invention relates to a novel mutant proteins having an amino acid
XX sequence that is different from and is at least about 70% identical to
XX the amino acid sequence of human receptor activator of Nf-kappaB (hRANK)
XX or human osteoprotegerin (hOPG), and which has a binding affinity to RANK
XX ligand (RANKL) that is at least as high as the binding affinity of hRANK
XX or hOPG to RANKL, as determined by functional competition assay. The
XX protein of the invention may have osteopathic activity and may act as a
XX RANKL-mediated osteoclastogenesis or RANKL-mediated osteoclast activity
XX inhibitor. The nucleotide sequence shown in the invention may be used in
XX gene therapy. The protein of the invention or fusion proteins comprising
XX this protein are useful as a pharmaceutical, and in the preparation of a
XX medicament for treating or preventing osteoporosis, or other bone
XX diseases or diseases associated with binding of RANKL to the RANK
XX receptor. A host cell containing a vector expressing the protein is
XX useful for producing a polypeptide having binding affinity to RANKL,
XX where the polypeptide comprises at least one N- or O-glycosylation site
XX and the host cell is a eukaryotic host cell capable of in vivo
XX glycosylation, and/or the polypeptide is subjected to conjugation to a
XX non-polypeptide moiety in vitro. The protein of the invention has
XX increased functional in vivo half-life and/or serum half-life compared to
XX hRANK or hOPG and has an improved binding affinity to RANKL compared to
XX the binding affinity of hRANK or hOPG to RANKL, as determined by a
XX functional competition assay. The present sequence represents the human
XX wild type OPG (osteoprotegerin) protein used to generate the mutant
XX proteins invention

XX Sequence 401 AA;
SQ
Query Match 100.0%; Score 2085; DB 5; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKHCTAKWTKVACPCPDHYTDSWHTSDECL 60
Db 22 ETPPKYLHYDEETSHQLCDKCPGTYLKHCTAKWTKVACPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQVVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTV 120
Db 82 YCSPVCKELQVVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTV 141
QY 121 CKRCPDFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDFFSNETS KAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLDNLP GTKVNAESVERIKRQHSOETQQLKLWKHQN 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLDNLP GTKVNAESVERIKRQHSOETQQLKLWKHQN 261
QY 241 KAQDIVKKIIQDIDL CENSQRHIGHANLTFEQLRSIMESLP GKVGAEDEKTIKACKP 300
Db 262 KAQDIVKKIIQDIDL CENSQRHIGHANLTFEQLRSIMESLP GKVGAEDEKTIKACKP 321
QY 301 SDQILKLLSLWRIKNGDQTLKGLMHALKHSTKYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGDQTLKGLMHALKHSTKYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNQVQSVKISL 380
Db 382 QKLFLEMIGNQVQSVKISL 401
RESULT 12
ABP55109
ID ABP55109 standard; protein; 401 AA.
XX
AC ABP55109;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human osteoprotegerin receptor.
XX
KW Osteoprotegerin; receptor; OPG; human; autoimmune disease;
KW rheumatoid arthritis; diabetes; osteoarthritis; psoriasis;
KW inflammatory bowel disease; transplant rejection; allergy;
KW immunosuppressive; antirheumatic; antiarthritic; antidiabetic;
KW antipsoriatic; immunosuppressive; antiallergic; antiinflammatory;
KW osteopathic; antitumor; monocytic.
XX
OS Homo sapiens.
XX WO200276507-A2.
XX
XX 03-OCT-2002.
XX
XX 06-FEB-2002; 2002WO-US001238.
XX
XX 23-MAR-2001; 2001US-0278215P.
XX
XX (GETH) GENENTECH INC.
XX
XX Grewal I;
XX
XX WPI; 2003-058352/05.
XX N-PSDB; ABV75843.
XX
XX Stimulating mammalian monocytes by exposing to an OPG ligand polypeptide,
XX useful for treating immune related disorders such as autoimmune disease,
XX rheumatoid arthritis, diabetes, osteoarthritis, psoriasis, and allergy.

XX Disclosure; Fig 2B; 11lpp; English.

PS The present sequence is the protein sequence of human osteoprotegerin

XX (OPG) receptor. The invention provides methods of using OPG ligand (OPGL)

CC to activate monocytes to secrete chemokines or cytokines by exposing a

CC mammalian cell (in cell culture or in a mammal) to OPGL. Also provided

CC are methods of using OPGL to treat conditions or diseases in mammals

CC associated with, or resulting from lack of, or decreased, chemokine or

CC cytokine secretion by monocytes. The invention also provides OPG agonist

CC and antagonist molecules to modulate immune activity. These may include

CC antibodies to the OPG or RANK receptors. An antagonist comprising an anti

CC -OPGL antibody, an anti-OPG receptor antibody, an anti-RANK receptor

CC antibody, an OPG receptor immunoadhesin or a RANK receptor immunoadhesin

CC is used in a claimed method of treating an immune-related condition,

CC especially an autoimmune disease, rheumatoid arthritis, insulin dependent

CC diabetes, osteoarthritis, inflammatory bowel disease (especially

CC ulcerative colitis or Crohn's disease), psoriasis, transplant rejection

CC or allergy

XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 2085; DB 6; Length 401;

Best Local Similarity 100.0%; Pred. No. 5.5e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETPFPKYLHYDETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 60

DB 22 ETPFPKYLHYDETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 81

QY 61 YGSPVCKELQYVKQECNTRHNVCCKEGRYLEIEFCLKHSRCPFGVGVQAGTPERNTV 120

DB 82 YGSPVCKELQYVKQECNTRHNVCCKEGRYLEIEFCLKHSRCPFGVGVQAGTPERNTV 141

QY 121 CKRCPDGFPSNETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 180

DB 142 CKRCPDGFPSNETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 201

QY 181 CSEAFRRFAVPKFTPNWLSVLVDNLPGLKVAESVERIKRQHSQEQTFQLLKLWKHQN 240

DB 202 CSEAFRRFAVPKFTPNWLSVLVDNLPGLKVAESVERIKRQHSQEQTFQLLKLWKHQN 261

QY 241 KQADIVKIIQDIDLCEMSVQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACP 300

DB 262 KQADIVKIIQDIDLCEMSVQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACP 321

QY 301 SQDILKLLSLWIKNGDQDTLKGMLHAKHSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 360

DB 322 SQDILKLLSLWIKNGDQDTLKGMLHAKHSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLEMIGNQVQSVKISCL 380

DB 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 13

AAE34363

ID AAE34363 standard; protein; 401 AA.

XX AAE34363;

AC AAE34363;

XX

DT 14-MAY-2003 (first entry)

XX Human osteoprotegerin (OPG) protein.

DE

XX Human; acute septic arthritis; osteomalacia; hyperparathyroidism;

KW Cushing's syndrome; receptor activator of NF-kappa B; cancer; scurvy;

KW bone formation; rickets; Langerhan's cell histiocytosis; gene therapy;

KW monocystotic fibrous dysplasia; radiation therapy; spinal cord injury;

KW RANK; Gaucher's disease; polycystotic fibrous dysplasia; OPG;

KW osteoprotegerin.

XX

OS Homo sapiens.

XX Key Location/Qualifiers

PH 1. .21

FT Peptide /label= Signal_peptide

FT Protein 22. .401

XX /note= "Mature OPG protein"

PN WO200292016-A2.

XX

PD 21-NOV-2002.

XX

PF 17-MAY-2002; 2002WO-US016002.

XX

PR 17-MAY-2001; 2001US-0291919P.

XX (IMNV) IMMUNEX CORP.

PA

XX Dougall WC, Anderson DM;

PI WPI; 2003-129220/12.

DR N-PSDB; AAD52597.

XX

PT Treating patients having e.g. acute septic arthritis, osteomalacia,

PT hyperparathyroidism, Cushing's syndrome or spinal cord injury, comprises

PT administering a receptor activator of NF-kappa B antagonist to increase

PT bone formation.

XX

PS Claim 1; Page 47-49; 52pp; English.

XX

CC The invention relates to a method of treating a patient having e.g. acute

CC septic arthritis, osteomalacia, hyperparathyroidism, Cushing's syndrome

CC or spinal cord injury. The method involves administering a receptor

CC activator of NF-kappa B (RANK) antagonist to stimulate an increase in the

CC rate for formation of new bone. RANK antagonist is capable of inhibiting

CC the ability of RANK to induce NF-kappa B. The method is useful for

CC stimulating bone formation, or for treating patients having acute septic

CC arthritis, osteomalacia (including rickets and scurvy),

CC hyperparathyroidism, Cushing's syndrome, monocystotic fibrous dysplasia,

CC polycystotic fibrous dysplasia, Gaucher's disease, Langerhan's cell

CC histiocytosis, spinal cord injury. Patients requiring periodontal

CC reconstruction, or patients who have completed a course or radiation

CC therapy for cancer. The method is also useful for treating a patient who

CC is a prosthetic joint recipient, a bone graft recipient, or a ligament

CC graft recipient. The invention is useful in gene therapy. The present

CC sequence is human osteoprotegerin (OPG). OPG serves as human RANK

CC antagonist

XX

SQ Sequence 401 AA;

Query Match 100.0%; Score 2085; DB 6; Length 401;

Best Local Similarity 100.0%; Pred. No. 5.5e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETPFPKYLHYDETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 60

DB 22 ETPFPKYLHYDETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 81

QY 61 YGSPVCKELQYVKQECNTRHNVCCKEGRYLEIEFCLKHSRCPFGVGVQAGTPERNTV 120

DB 82 YGSPVCKELQYVKQECNTRHNVCCKEGRYLEIEFCLKHSRCPFGVGVQAGTPERNTV 141

QY 121 CKRCPDGFPSNETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 180

DB 142 CKRCPDGFPSNETSKAPCKRHTNCSVFGLLLTQKGNATHDNCISGNSSESTOKCGIDVTL 201

QY 181 CSEAFRRFAVPKFTPNWLSVLVDNLPGLKVAESVERIKRQHSQEQTFQLLKLWKHQN 240

DB 202 CSEAFRRFAVPKFTPNWLSVLVDNLPGLKVAESVERIKRQHSQEQTFQLLKLWKHQN 261

QY 241 KQADIVKIIQDIDLCEMSVQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACP 300

DB 262 KQADIVKIIQDIDLCEMSVQRHGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACP 321

QY 301 SDQILKLLSLWRIKNGDQDTLKGIMALKHKSHTYHFPKVTQSLKKTIRFLHSFTMYKLY 360
 DB 322 SDQILKLLSLWRIKNGDQDTLKGIMALKHKSHTYHFPKVTQSLKKTIRFLHSFTMYKLY 381
 QY 361 QKLFLFLEMIGNQVQSVKISCL 380
 DB 382 QKLFLFLEMIGNQVQSVKISCL 401

RESULT 14
 ADD01627
 ID ADD01627 standard; protein; 401 AA.
 XX
 AC ADD01627;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human osteoprotegerin amino acid sequence SEQ ID NO:4.
 XX
 KW fibrotic disease; cysteine-rich domain; osteoprotegerin; scleroderma;
 KW antiinflammatory; gene therapy; human.
 XX
 OS Homo sapiens.
 XX
 PN WO2003084560-A2.
 XX
 PD 16-OCT-2003.
 XX
 PF 26-MAR-2003; 2003WO-EP050080.
 XX
 PR 10-APR-2002; 2002EP-00100364.
 XX
 PA (ISTP) ARS APPLIED RES SYSTEMS HOLDING NV.
 XX
 PI Power C, Plater-Zyberk C;
 XX
 DR WPI; 2003-804248/75.
 DR N-PSDB; ADD01626.
 XX
 PT Use of a substance for the manufacture of a medicament for treating or
 PT preventing fibrotic disease.
 XX
 PS Claim 1; SEQ ID NO 4; 68pp; English.
 XX
 CC The present invention describes a substance which is useful for the
 CC manufacture of a medicament for treating or preventing fibrotic disease.
 CC The substance comprises: (a) a polypeptide comprising a fully defined
 CC sequence having 401 amino acids (see ADD01625 and ADD01627), or its amino
 CC acids 22-401 or 22-194; (b) a polypeptide comprising 1, 2, 3 or 4
 CC cysteine-rich domains of osteoprotegerin; (c) a mutin of (a)-(b) that is
 CC encoded by a DNA sequence that hybridises to the complement of the DNA
 CC sequence encoding (a)-(b) under moderately or highly stringent conditions
 CC ; where the amino acid sequence has at least 40, 50, 60, 70, 80 or 90%
 CC identity with (a)-(b); and where any changes in the amino acid sequence
 CC are conservative amino acid substitutions to the amino acid sequences in
 CC (a)-(b); or (d) a salt or an isoform, fused protein, functional
 CC derivative, active fraction or circularly permuted derivative of (a)-
 CC (c). Also described: (1) a polypeptide comprising the 401-amino acid
 CC sequence and one, two, three or four cysteine-rich domains of
 CC osteoprotegerin; and (2) a method for treating or preventing a fibrotic
 CC disease, particularly scleroderma. The substance has antiinflammatory
 CC activity, and can be used in gene therapy. A vector or cell comprising
 CC the nucleic acid molecule encoding a polypeptide of the invention can be
 CC used for inducing or enhancing the endogenous production of the
 CC polypeptide in a cell for the preparation of a medicament for treating or
 CC preventing a fibrotic disease, in particular scleroderma. The present
 CC sequence represents a human osteoprotegerin amino acid sequence which is
 CC used in the exemplification of the present invention.

XX SQ Sequence 401 AA;
 Query Match 100.0%; Score 2085; DB 7; Length 401;
 Best Local Similarity 100.0%; Pred. No. 5.5e-153;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPFKYLYHDETSQHLCDKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 DB 22 ETFPFKYLYHDETSQHLCDKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
 QY 61 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERTV 120
 DB 82 YCSPVCKELQYVQKQECNRTHNRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERTV 141
 QY 121 CKRCPDGFFSNETSAPCKRKTNCVSFGLLLTQKGNATHDNCISGNSESTQKCGIDVTL 180
 DB 142 CKRCPDGFFSNETSAPCKRKTNCVSFGLLLTQKGNATHDNCISGNSESTQKCGIDVTL 201
 QY 181 CEEAFFRAVPTKFTENWLSVLVDNLPGTKVNAESVERIKRQHSOBOQFOLLKLWKQON 240
 DB 202 CEEAFFRAVPTKFTENWLSVLVDNLPGTKVNAESVERIKRQHSOBOQFOLLKLWKQON 261
 QY 241 KAQDIVKKIIQIDILCENSQVRHIGHANLTFEQLRSIMESLPCKVKYGAEDIEKTIKACP 300
 DB 262 KAQDIVKKIIQIDILCENSQVRHIGHANLTFEQLRSIMESLPCKVKYGAEDIEKTIKACP 321
 QY 301 SDQILKLLSLWRIKNGDQDTLKGIMALKHKSHTYHFPKVTQSLKKTIRFLHSFTMYKLY 360
 DB 322 SDQILKLLSLWRIKNGDQDTLKGIMALKHKSHTYHFPKVTQSLKKTIRFLHSFTMYKLY 381
 QY 361 QKLFLFLEMIGNQVQSVKISCL 380
 DB 382 QKLFLFLEMIGNQVQSVKISCL 401

RESULT 15
 ADM28813
 ID ADM28813 standard; protein; 401 AA.
 XX
 AC ADM28813;
 XX
 DT 20-MAY-2004 (first entry)
 XX
 DE Human osteoprotegerin, OPG.
 XX
 KW Human; OPG; bone resorption; excessive bone loss; osteoporosis;
 KW Paget's disease of bone; hypercalcaemia; hyperparathyroidism;
 KW steroid-induced osteopaenia; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; Cushing's syndrome;
 KW acromegaly; osteogenesis imperfecta; homocystinuria; Menke's syndrome;
 KW Riley-day syndrome; immobilisation of extremity; tumour;
 KW haematologic malignancy; multiple myeloma; lymphoma; leukaemia;
 KW renal function disorder; osteopaenia; osteonecrosis; bone cell death;
 KW osteoprotegerin; transgenic.
 XX
 OS Homo sapiens.

Key Location/Qualifiers
 Peptide 1..21
 Protein 22..401
 Region 22..201
 Region 22..194
 Region 22..189
 Region 22..185
 Region 27..401
 Region 27..194
 Region 27..189
 Region 27..185

/note= "Signal peptide"
 /note= "Mature OPG, claimed in claim 24"
 /note= "Claimed in claim 32"
 /note= "Claimed in claim 32"
 /note= "Claimed in claim 32"
 /note= "Claimed in claim 32"
 /note= "Claimed in claim 35"
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 /note= "Claimed in claim 35"
 /note= "Claimed in claim 35"

FT /note= "Claimed in claim 35"
FT 32. .401
XX /note= "Claimed in claim 25"
XX
PN US2003207827-A1.
XX
PD 06-NOV-2003.
XX
XX
PF 24-SEP-1999; 99US-00405032.
XX
PR 22-DEC-1995; 95US-00577798.
PR 03-SEP-1996; 96US-00706945.
PR 20-DEC-1996; 96US-00771777.
PR 12-AUG-1998; 98US-00132985.
XX
PA (BOYL/) BOYLE W J.
PA (LACE/) LACEY D L.
PA (CALZ/) CALZONE F J.
PA (CHAN/) CHANG M.
XX
PI Boyle WJ, Lacey DL, Calzone FJ, Chang M;
XX
XX WPI; 2004-041572/04.
DR N-PSDB; ADM28812.
XX
XX Novel osteoprotegerin useful for treating conditions resulting in bone
PT loss such as osteoporosis, hypercalcaemia, Paget's disease of bone, bone
PT loss caused by rheumatoid arthritis or osteomyelitis.
XX
XX Claim 23; SEQ ID NO 125; 141pp; English.
XX
XX The invention relates to a purified and isolated polypeptide having
CC osteoprotegerin (OPG), an OPG polypeptide from rat, human and mouse, or
CC having amino terminus at residue 22, and 1-216 amino acids are deleted
CC from carboxy terminus of human OPG polypeptide. Also included are an
CC isolated nucleic acid encoding an OPG polypeptide (OPG NA), an expression
CC vector, a transgenic mammal comprising the cell, producing OPG, a
CC polypeptide comprising an amino acid sequence of at least about 164 amino
CC acids comprising four cysteine-rich domains characteristic of the
CC cysteine rich domains of tumour necrosis factor receptor extracellular
CC regions (and an activity of increasing bone density), an antibody (Ab) or
CC its fragment which specifically binds to OPG, a composition comprising
CC OPG (in a carrier, adjuvant, solubiliser, stabiliser and/or anti-oxidant)
CC and an osteoprotegerin multimer consisting of osteoprotegerin monomers.
CC Ab is useful for detecting the presence of OPG in a biological sample
CC which involves incubating the sample with Ab under conditions that allow
CC binding of ab to OPG and detecting the bound Ab. OPG is useful for
CC assessing the ability of a candidate substance to bind to OPG. OPG NA is
CC useful for regulating the levels of OPG in an animal (human). The nucleic
CC acid promotes an increasing in tissue level of OPG. OPG is useful for
CC treating a bone disorder e.g. excessive bone loss, osteoporosis, Paget's
CC disease of bone, hypercalcaemia, hyperparathyroidism, steroid-induced
CC osteopaenia, bone loss due to rheumatoid arthritis, bone loss due to
CC osteomyelitis, osteolytic metastasis, and periodontal bone loss. The
CC method further involves administering a substance chosen from bone
CC morphogenic protein BMP-1 through BMP-12, TGF-beta family members, IL-1
CC inhibitor, TNFalpha inhibitors, parathyroid hormone and their analogues,
CC parathyroid hormone related protein and their analogues, E series of
CC prostaglandins, bisphosphonates, and bone-enhancing minerals. OPG is
CC useful for treating osteoporosis such as primary osteoporosis, endocrine
CC osteoporosis (hyperthyroidism, Cushing's syndrome, and acromegaly),
CC hereditary and congenital forms of osteoporosis (osteogenesis imperfecta
CC, homocystinuria, Menke's syndrome, and Riley-day syndrome) and
CC osteoporosis due to immobilisation of extremities, hypercalcaemia
CC resulting from solid tumours and haematologic malignancies (multiple
CC myeloma, lymphoma and leukaemia), idiopathic hypercalcaemia, and
CC hypercalcaemia associated with hyperthyroidism and renal function
CC disorders, osteopaenia following surgery and osteonecrosis or bone cell
CC death. The present sequences is an OPG protein (or fragment).
XX
XX Sequence 401 AA;

Query Match 100.0%; Score 2085; DS 8; Length 401;
Best Local Similarity 100.0%; Pred. No. 5.5e-153;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFFPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCDPHYTTDSWHTSDECL 60
Db 22 ETFFPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCDPHYTTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQCNRTHRVCECKRGYLEIEFCLKHRSCPPGFGVQAGTPERTV 120
Db 82 YCSPVCKELQYVKQCNRTHRVCECKRGYLEIEFCLKHRSCPPGFGVQAGTPERTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCVFGLLLTQKGNATHDNCISGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCVFGLLLTQKGNATHDNCISGNSESTQKCGIDVTL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSQRTFQLLKLWKHQN 240
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QY 301 SDQILKLLSLWRIKNGDDDTLLKGLMEALKHKSCTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
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QY 361 QKLFLEMIQNOVQSVKISCL 380
Db 382 QKLFLEMIQNOVQSVKISCL 401

Search completed: November 15, 2004, 19:00:32
Job time : 164 secs

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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:51:06 ; Search time 47 Seconds
(without alignments)
536.188 Million cell updates/sec

Title: US-10-676-358-1

Perfect score: 2085

Sequence: 1 ETFPKYLHYDETHSHQLL.....QKLFLEMGVQSVKISCL 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:*
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4: /cgn2_6/protdata/1/iaa/6B COMB.pep.*
5: /cgn2_6/protdata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/protdata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2085	100.0	401	3	US-08-974-022-6
2	2085	100.0	401	3	US-09-042-785A-12
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4	2085	100.0	401	3	US-08-795-447A-6
5	2085	100.0	401	3	US-08-974-186-6
6	2085	100.0	401	3	US-08-795-446B-6
7	2085	100.0	401	3	US-08-706-945D-128
8	2085	100.0	401	4	US-08-577-788C-6
9	2085	100.0	401	4	US-08-577-788C-56
10	2085	100.0	401	4	US-09-064-832-2
11	2079	99.7	401	3	US-09-153-927-1
12	2079	99.7	401	3	US-09-072-993C-1
13	1982	95.1	364	3	US-08-706-945D-142
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18	1828	87.7	401	3	US-08-795-446B-2
19	1828	87.7	401	3	US-08-706-945D-124
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21	1828	87.7	401	4	US-08-577-788C-55
22	1820	87.3	401	3	US-08-974-022-4
23	1820	87.3	401	3	US-09-042-785A-13
24	1820	87.3	401	3	US-08-795-445A-4
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28 1820 87.3 401 3 US-08-706-945D-126
29 1820 87.3 401 4 US-08-577-788C-4
30 1820 87.3 401 4 US-08-577-788C-54
31 1720 82.5 364 3 US-08-706-945D-141
32 1531 73.4 293 4 US-09-896-096A-18
33 952 45.7 208 4 US-08-577-788C-50
34 945 45.3 161 4 US-09-632-277A-3
35 865 41.5 147 3 US-09-527-236A-20
36 865 41.5 147 4 US-09-527-236A-20
37 861 41.3 146 4 US-09-523-323-58
38 827 39.7 139 3 US-08-706-945D-130
39 781 37.5 174 3 US-08-706-945D-136
40 440.5 21.1 300 2 US-08-794-796-2
41 440.5 21.1 300 4 US-09-632-277A-2
42 440.5 21.1 300 4 US-09-523-323-52
43 440.5 21.1 300 4 US-09-896-096A-1
44 433 20.8 211 3 US-09-286-529-20
45 432 20.7 299 3 US-09-286-529-17

ALIGNMENTS

RESULT 1

US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-6

Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 82 YCSFVKELQVQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNTV 141
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTOKGNATHNICSNSESTOKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTOKGNATHNICSNSESTOKCGIDVTL 201
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Db 202 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKQHSSESTOKCGIDVTL 261
Qy 241 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 300
Db 262 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 321
Qy 301 SDQILKLLSLWRIKNGDQDTLKGMLHALKHSKTVHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGDQDTLKGMLHALKHSKTVHFPKTVTQSLKKTIRFLHSFTMYKLY 381
Qy 361 OKLFLEMIGNOVQSVKISCL 380
Db 382 OKLFLEMIGNOVQSVKISCL 401

RESULT 2
US-09-042-785A-12
; Sequence 12, Application US/09042785A
; Patent No. 6194151
; GENERAL INFORMATION:
; APPLICANT: Busfield, Samantha J
; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSES: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/042,785A
; FILING DATE: 17-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/938,896
; FILING DATE: 26-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-001CP
; TELEPHONE: (617) 227-7400
; TELEFAX: (617) 742-4214
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-042-785A-12

Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ETFFPKYLVHDETSQHLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFFPKYLVHDETSQHLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
Qy 61 YCSFVKELQVQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNTV 120
Db 82 YCSFVKELQVQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVQAGTPERNTV 141
Qy 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTOKGNATHNICSNSESTOKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTOKGNATHNICSNSESTOKCGIDVTL 201
Qy 181 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKQHSSESTOKCGIDVTL 240
Db 202 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKQHSSESTOKCGIDVTL 261
Qy 241 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 300
Db 262 KAQDIVVKIIQDIDLCEMSVQRHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACP 321
Qy 301 SDQILKLLSLWRIKNGDQDTLKGMLHALKHSKTVHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGDQDTLKGMLHALKHSKTVHFPKTVTQSLKKTIRFLHSFTMYKLY 381
Qy 361 OKLFLEMIGNOVQSVKISCL 380
Db 382 OKLFLEMIGNOVQSVKISCL 401

RESULT 3
US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-445A-6

Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ETFFPKYLVHDETSQHLLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTKVCAPCPDHYTDSWHTSDECL 81
YQ 61 YCSPVCKELQVVKOECHNRTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNTV 120
Db 82 YCSPVCKELQVVKOECHNRTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNTV 141
YQ 121 CKRCPDFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
YQ 181 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSESTQKCGIDVTL 240
Db 202 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSESTQKCGIDVTL 261
YQ 241 KAODIVVKIIQDIDLDCNSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAODIVVKIIQDIDLDCNSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
YQ 301 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 381
YQ 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 4

US-08-795-447A-6

; Sequence 6, Application US/08795447A

; Patent No. 6284728

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: Osteoprotegerin

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: One Amgen Center Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91362-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/795,447A

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-378D2

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 401 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-795-447A-6

Query Match

Best Local Similarity 100.0%; Score 2085; DB 3; Length 401;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 ETFFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTKVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTKVCAPCPDHYTDSWHTSDECL 81

YQ 61 YCSPVCKELQVVKOECHNRTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNTV 120
Db 82 YCSPVCKELQVVKOECHNRTHNRVCEKGRYLEIEFCLKHSRCPGPGVQAGTPERNTV 141
YQ 121 CKRCPDFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
YQ 181 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSESTQKCGIDVTL 240
Db 202 CEEAFFPAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKQHSSESTQKCGIDVTL 261
YQ 241 KAODIVVKIIQDIDLDCNSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAODIVVKIIQDIDLDCNSVQRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
YQ 301 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGQDQTLKGLMHALKHSKTYHFFPKTYTQSLKKTIRFLHSFTMYKLY 381
YQ 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 5

US-08-974-186-6

; Sequence 6, Application US/08974186

; Patent No. 6284740

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; APPLICANT: Chang, Ming-Shi

; TITLE OF INVENTION: Osteoprotegerin

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Amgen Inc.

; STREET: 1840 Dehavilland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: IBM PC compatible

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/974,186

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/577,788

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-378

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 401 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-974-186-6

Query Match

Best Local Similarity 100.0%; Score 2085; DB 3; Length 401;

Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

YQ 1 ETFFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTKVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 120
Db 82 YCSPVCKELQYVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOQTFOQLKLWKHQH 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOQTFOQLKLWKHQH 261
QY 241 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRIKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 6

US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Behavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-446B-6
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60

Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 120
Db 82 YCSPVCKELQYVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOQTFOQLKLWKHQH 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOQTFOQLKLWKHQH 261
QY 241 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
Db 262 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRIKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 7

US-08-706-945D-128
; Sequence 128, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; CURRENT FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 128
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-706-945D-128
Query Match 100.0%; Score 2085; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 120
Db 82 YCSPVCKELQYVKQECNTHNRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOQTFOQLKLWKHQH 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPCTKVNAESVERIKRQHSQEOQTFOQLKLWKHQH 261
QY 241 KAQDIVKKIIQDIDL CENSQVORHIGHANLTPEQLRSLMESLPGKKVGAEDIEKTIKACKP 300

Db 262 KAQDIVKKIIQIDLNCNSVQRHIGHANLTFEQLRSIMESLPKKVGAEDIEKTIKACP 321
QY 301 SDQILKLSLWRINKGDDTLKGLMHALKHSKTYHPKTVTQSLKKTIRFLHSFTWKLY 360
Db 322 SDQILKLSLWRINKGDDTLKGLMHALKHSKTYHPKTVTQSLKKTIRFLHSFTWKLY 381
QY 361 QKLFLMIGNQVQSVKISCL 380
Db 382 QKLFLMIGNQVQSVKISCL 401

RESULT 8
US-08-577-788C-6
; Sequence 6, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-577-788C-6

Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 120
Db 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQCGIDVTL 201
QY 181 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQ 240
Db 202 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQ 261
QY 241 KAQDIVKKIIQIDLNCNSVQRHIGHANLTFEQLRSIMESLPKKVGAEDIEKTIKACP 300
Db 262 KAQDIVKKIIQIDLNCNSVQRHIGHANLTFEQLRSIMESLPKKVGAEDIEKTIKACP 321
QY 301 SDQILKLSLWRINKGDDTLKGLMHALKHSKTYHPKTVTQSLKKTIRFLHSFTWKLY 360
Db 322 SDQILKLSLWRINKGDDTLKGLMHALKHSKTYHPKTVTQSLKKTIRFLHSFTWKLY 381
QY 361 QKLFLMIGNQVQSVKISCL 380
Db 382 QKLFLMIGNQVQSVKISCL 401

RESULT 9
US-08-577-788C-56
; Sequence 56, Application US/08577788C
; Patent No. 6613544
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank

; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378 Rev
; CURRENT APPLICATION NUMBER: US/08/577,788C
; CURRENT FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 56
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-577-788C-56

Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLLCKPCPGTYLKQCHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 120
Db 82 YCSPVCKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVVQAGTPERTV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCNSGSESTQCGIDVTL 201
QY 181 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQ 240
Db 202 CEEAFFRAVPTKFTFNWLSVLVDNLPGTKVNAESVERIKRQHSSEQOTFQLLKLWKHQ 261
QY 241 KAQDIVKKIIQIDLNCNSVQRHIGHANLTFEQLRSIMESLPKKVGAEDIEKTIKACP 300
Db 262 KAQDIVKKIIQIDLNCNSVQRHIGHANLTFEQLRSIMESLPKKVGAEDIEKTIKACP 321
QY 301 SDQILKLSLWRINKGDDTLKGLMHALKHSKTYHPKTVTQSLKKTIRFLHSFTWKLY 360
Db 322 SDQILKLSLWRINKGDDTLKGLMHALKHSKTYHPKTVTQSLKKTIRFLHSFTWKLY 381
QY 361 QKLFLMIGNQVQSVKISCL 380
Db 382 QKLFLMIGNQVQSVKISCL 401

RESULT 10
US-09-064-832-2
; Sequence 2, Application US/09064832
; Patent No. 6790823
; GENERAL INFORMATION:
; APPLICANT: Simonet, Scott
; APPLICANT: Sarosi, Ildiko
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: PREVENTION AND TREATMENT OF CARDIOVASCULAR DISEASES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/064,832
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-064-832-2

Query Match 100.0%; Score 2085; DB 4; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.4e-186;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 120
DB 82 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 201

QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
DB 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 261

QY 241 KAQDIVVKIIQDIDL CENSQVQRHIGHANLTPEQLRS LMESLP GKXVGAEDIEKTIKACKP 300
DB 262 KAQDIVVKIIQDIDL CENSQVQRHIGHANLTPEQLRS LMESLP GKXVGAEDIEKTIKACKP 321

QY 301 SDQILKLLSLWRIKNGDQDTLGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRIKNGDQDTLGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 11
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
US-09-153-927-1

Query Match 99.7%; Score 2079; DB 3; Length 401;
Best Local Similarity 99.7%; Pred. No. 8.5e-186;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 120
DB 82 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 201

QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
DB 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 261

DB 22 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 120
DB 82 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 201
QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
DB 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 261
QY 241 KAQDIVVKIIQDIDL CENSQVQRHIGHANLTPEQLRS LMESLP GKXVGAEDIEKTIKACKP 300
DB 262 KAQDIVVKIIQDIDL CENSQVQRHIGHANLTPEQLRS LMESLP GKXVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRIKNGDQDTLGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRIKNGDQDTLGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 12
US-09-072-993C-1
; Sequence 1, Application US/09072993C
; Patent No. 6346388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham-Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TR1 AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1

Query Match 99.7%; Score 2079; DB 3; Length 401;
Best Local Similarity 99.7%; Pred. No. 8.5e-186;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETFPPKYLHYDEETSHQLLCKCPGTYLKHCTAKWKTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 120
DB 82 YCSPVKELQYVQECNRTNHRVCECKEGRYLEIEFCLKHRSCTPPGFGVQAGTPERNIV 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTI 180
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QY 181 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 240
DB 202 CEEAFFRFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHON 261

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QY 301 SDQILKLLSWRIKNGDQDITLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSWRIKNGDQDITLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLFLEMIGNQVQSVKISCL 401

RESULT 13
US-08-706-945D-142
; Sequence 142, Application US/08706945D
; Patent No. 6369027
; GENERAL INFORMATION:
; APPLICANT: Boyle, William
; APPLICANT: Lacey, David
; APPLICANT: Calzone, Frank
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; FILE REFERENCE: A-378CIP
; CURRENT APPLICATION NUMBER: US/08/706,945D
; PRIOR FILING DATE: 1996-09-03
; PRIOR APPLICATION NUMBER: 08/577,788
; PRIOR FILING DATE: 1995-12-22
; NUMBER OF SEQ ID NOS: 145
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 142
; LENGTH: 364
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-706-945D-142
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Best Local Similarity 95.8%; Pred. No. 8.6e-177;
Matches 364; Conservative 0; Mismatches 0; Indels 16; Gaps 1;

QY 1 ETEPPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 1 ETEPPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
QY 61 YCSPVKELQYVQECNRTNRHVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 120
Db 61 YCSPVKELQYVQECNRTNRHVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 120
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Db 121 CKRCPDGFFSNETSAPCRKHTN-----DNICSGNSESTQKCGIDVTL 164
QY 181 CEEAFFRFAVPTFTFNWLSVLVDNLPGTKVNAESVERIKRQHSOQOTFOLLKLWKHQN 240
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Db 225 KAQDIVKKIIQIDILCENSQVORHIGHANLTFEQLRSIMESLPKGGKGAEDIEKTIKACP 284
QY 301 SDQILKLLSWRIKNGDQDITLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
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QY 361 QKLFLFLEMIGNQVQSVKISCL 380
Db 345 QKLFLFLEMIGNQVQSVKISCL 364
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RESULT 14
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
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; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-974-022-2

Query Match 87.7%; Score 1828; DB 3; Length 401;
Best Local Similarity 86.3%; Pred. No. 2.4e-162;
Matches 328; Conservative 24; Mismatches 28; Indels 0; Gaps 0;

QY 1 ETEPPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETEPPKYLHYDEETSHQLLCKPCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVKELQYVQECNRTNRHVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 120
Db 82 YCSPVKELQYVQECNRTNRHVCECKEGRYLEIEFCLKHSRCPGPGVVOAGTPERNTV 141
QY 121 CKRCPDGFFSNETSAPCRKHTNCSVFGLLLTQKGNATHDNCNCSGSESTQKCGIDVTL 180
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QY 181 CEEAFFRFAVPTFTFNWLSVLVDNLPGTKVNAESVERIKRQHSOQOTFOLLKLWKHQN 240
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QY 301 SDQILKLLSWRIKNGDQDITLKGIMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SEOLLKLLSWRIKNGDQDITLKGIMYALKHLYKAYHFPKTVTTHSLRKTIRFLHSFTMYRLY 381
QY 361 QKLFLFLEMIGNQVQSVKISCL 380
Db 382 QKLFLFLEMIGNQVQSVKISCL 401
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RESULT 15
US-08-795-445A-2
; Sequence 2, Application US/08795445A
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:54:37 ; Search time 145 Seconds
(without alignments)
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Title: US-10-676-358-1

Perfect score: 2085

Sequence: 1 ETFPKYLHYDEBTHQLLC.....QKLFLEMIGNQVQSVKISCL 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters: 1568699

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	2085	100.0	380	10	US-09-405-032-139	Sequence 139, Appl
2	2085	100.0	380	16	US-10-676-358-1	Sequence 1, Appli
3	2085	100.0	400	14	US-10-142-658-2	Sequence 2, Appli
4	2085	100.0	401	10	US-09-405-032-125	Sequence 125, Appl
5	2085	100.0	401	14	US-10-151-071-8	Sequence 8, Appli
6	2085	100.0	401	16	US-10-467-243-2	Sequence 2, Appli
7	2085	100.0	537	16	US-10-676-358-6	Sequence 6, Appli
8	2079	99.7	380	9	US-09-062-113-4	Sequence 4, Appli
9	2079	99.7	380	14	US-10-232-858-4	Sequence 4, Appli
10	2079	99.7	380	16	US-10-785-109-4	Sequence 4, Appli
11	2079	99.7	380	16	US-10-785-109-4	Sequence 4, Appli
12	2079	99.7	391	9	US-10-785-114-4	Sequence 106, Appl
13	2079	99.7	391	14	US-10-232-858-106	Sequence 106, Appl

14	2079	99.7	391	16	US-10-785-109-106	Sequence 106, App
15	2079	99.7	391	16	US-10-785-114-106	Sequence 106, App
16	2079	99.7	401	9	US-09-062-113-5	Sequence 5, Appli
17	2079	99.7	401	13	US-10-039-785-5	Sequence 5, Appli
18	2079	99.7	401	13	US-10-066-209-1	Sequence 1, Appli
19	2079	99.7	401	13	US-10-105-934-2	Sequence 2, Appli
20	2079	99.7	401	13	US-10-164-592-2	Sequence 2, Appli
21	2079	99.7	401	14	US-10-183-091-1	Sequence 1, Appli
22	2079	99.7	401	14	US-10-364-045-1	Sequence 1, Appli
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39	2069	99.2	401	14	US-10-232-858-66	Sequence 66, Appli
40	2069	99.2	401	16	US-10-785-109-62	Sequence 62, Appli
41	2069	99.2	401	16	US-10-785-109-63	Sequence 63, Appli
42	2069	99.2	401	16	US-10-785-109-64	Sequence 64, Appli
43	2069	99.2	401	16	US-10-785-109-65	Sequence 65, Appli
44	2069	99.2	401	16	US-10-785-109-66	Sequence 66, Appli
45	2069	99.2	401	16	US-10-785-114-62	Sequence 62, Appli

ALIGNMENTS

RESULT 1

US-09-405-032-139
; Sequence 139, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 380 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 139:
US-09-405-032-139

Query Match	100.0%;	Score 2085;	DB 10;	Length 380;	
Best Local Similarity	100.0%;	Pred. No. 2.9e-167;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 380;	Conservative	0;			
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Db	1	ETFPKYLHYDEETSHQLL	CDKCPGTYLKQHCTAKWKTV	CAPCPDHYTDSWHTSDECL	60
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Db	181	CEEAFFRAVPTKFTPNW	LSVLVDNLPGTKVNAESVERI	KQHSQSQDTFQLLKLWKHQ	240
QY	241	KAQDIVKKIIQDIDL	CENSQVQRHIGHANLTFEQL	RSIMESLPKGGKVGAEDEIKTIKACP	300
Db	241	KAQDIVKKIIQDIDL	CENSQVQRHIGHANLTFEQL	RSIMESLPKGGKVGAEDEIKTIKACP	300
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Db	301	SDQILKLLSLWRKNG	QDQTLKGLMHALKHSTYH	FPKTVTQSLKKTIRFLHSFTMYKLY	360
QY	361	QKLFLEMIGNQVQSV	KISCL	380	
Db	361	QKLFLEMIGNQVQSV	KISCL	380	
RESULT 3					
US-10-142-658-2					
; Sequence 2, Application US/10142658					
; Publication No. US20030022834A1					
; GENERAL INFORMATION:					
; APPLICANT: Malyankar, Uriel M.					
; APPLICANT: Scatena, Marta					
; APPLICANT: Giachelli, Cecilia M.					
; TITLE OF INVENTION: METHODS AND DEVICES FOR PROMOTING ENDOTHELIAL MORPHOGENESIS					
; FILE REFERENCE: UMOT1118975					
; CURRENT APPLICATION NUMBER: US/10/142,658					
; CURRENT FILING DATE: 2002-05-09					
; PRIOR APPLICATION NUMBER: US 60/290,230					
; PRIOR FILING DATE: 2001-05-10					
; NUMBER OF SEQ ID NOS: 2					
; SOFTWARE: PatentIn version 3.1					
; SEQ ID NO 2					
; LENGTH: 400					
; TYPE: PRT					
; ORGANISM: Homo Sapiens					
US-10-142-658-2					
Query Match	100.0%;	Score 2085;	DB 14;	Length 400;	
Best Local Similarity	100.0%;	Pred. No. 3.1e-167;	Mismatches 0;	Indels 0;	Gaps 0;
Matches 380;	Conservative	0;			
QY	1	ETFPKYLHYDEETSHQLL	CDKCPGTYLKQHCTAKWKTV	CAPCPDHYTDSWHTSDECL	60
Db	21	ETFPKYLHYDEETSHQLL	CDKCPGTYLKQHCTAKWKTV	CAPCPDHYTDSWHTSDECL	80
QY	61	YCSPVCKELQYVQKQECNR	THNRVCECKEGRYLEIEFCL	KHRSCTPGFGVQAGTPERTV	120
Db	81	YCSPVCKELQYVQKQECNR	THNRVCECKEGRYLEIEFCL	KHRSCTPGFGVQAGTPERTV	140
QY	121	CKRCPDGFSSNETSSKAP	CRKHTNCSVFGLLTQKGNATH	DNICSGNSESTQKCGIDVTL	180
Db	141	CKRCPDGFSSNETSSKAP	CRKHTNCSVFGLLTQKGNATH	DNICSGNSESTQKCGIDVTL	200
QY	181	CEEAFFRAVPTKFTPNW	LSVLVDNLPGTKVNAESVERI	KQHSQSQDTFQLLKLWKHQ	240
Db	201	CEEAFFRAVPTKFTPNW	LSVLVDNLPGTKVNAESVERI	KQHSQSQDTFQLLKLWKHQ	260
QY	241	KAQDIVKKIIQDIDL	CENSQVQRHIGHANLTFEQL	RSIMESLPKGGKVGAEDEIKTIKACP	300
Db	261	KAQDIVKKIIQDIDL	CENSQVQRHIGHANLTFEQL	RSIMESLPKGGKVGAEDEIKTIKACP	320
QY	301	SDQILKLLSLWRKNG	QDQTLKGLMHALKHSTYH	FPKTVTQSLKKTIRFLHSFTMYKLY	360
Db	321	SDQILKLLSLWRKNG	QDQTLKGLMHALKHSTYH	FPKTVTQSLKKTIRFLHSFTMYKLY	380
QY	361	QKLFLEMIGNQVQSV	KISCL	380	
Db	381	QKLFLEMIGNQVQSV	KISCL	400	
RESULT 4					
US-09-405-032-125					

```

; Sequence 125, Application US/09405032
; Publication No. US20030207827A1
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 168
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: United States
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/405,032
; FILING DATE: 24-Sep-1999
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Wincer, Robert B.
; REFERENCE/DOCKET NUMBER: A-378-CIP2
; INFORMATION FOR SEQ ID NO: 125:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-405-032-125

Query Match 100.0%; Score 2085; DB 10; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 120
DB 82 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 261
QY 241 KAQDIVKKLIQIDILCENSVOQRHIGHANLTFEQLRSIMESLPKGVKYGABEDIKTIKACP 300
DB 262 KAQDIVKKLIQIDILCENSVOQRHIGHANLTFEQLRSIMESLPKGVKYGABEDIKTIKACP 321
QY 301 SQIILKLLSLWRKNGDQDTLKLMLHAKHSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SQIILKLLSLWRKNGDQDTLKLMLHAKHSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 382 QKLFLFMIGNQVQSVKISCL 401

RESULT 5
US-10-151-071-8
; Sequence 8, Application US/10151071
; Publication No. US20030017151A1
; GENERAL INFORMATION:
; APPLICANT: DOUGALL, William

```

```

; APPLICANT: ANDERSON, Dirk
; TITLE OF INVENTION: THERAPEUTIC USES OF RANK ANTAGONISTS
; FILE REFERENCE: 3277-A
; CURRENT APPLICATION NUMBER: US/10/151,071
; PRIOR FILING DATE: 2001-05-17
; PRIOR APPLICATION NUMBER: 60/291,919
; PRIOR FILING DATE: 2001-05-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 8
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-071-8

Query Match 100.0%; Score 2085; DB 14; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLCKDCPPGTYLKQHTAKWKTVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 120
DB 82 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGVGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNCISGNSSESTQKCGIDVTL 201
QY 181 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 240
DB 202 CEEAFFRAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSESTQKCGIDVTL 261
QY 241 KAQDIVKKLIQIDILCENSVOQRHIGHANLTFEQLRSIMESLPKGVKYGABEDIKTIKACP 300
DB 262 KAQDIVKKLIQIDILCENSVOQRHIGHANLTFEQLRSIMESLPKGVKYGABEDIKTIKACP 321
QY 301 SQIILKLLSLWRKNGDQDTLKLMLHAKHSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SQIILKLLSLWRKNGDQDTLKLMLHAKHSKTYHPKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLFMIGNQVQSVKISCL 380
DB 382 QKLFLFMIGNQVQSVKISCL 401

RESULT 6
US-10-467-243-2
; Sequence 2, Application US/10467243
; Publication No. US20040132971A1
; GENERAL INFORMATION:
; APPLICANT: Maxygen Holdings Ltd.
; APPLICANT: Haaning, Jesper Mortensen
; APPLICANT: Halkier, Torben
; TITLE OF INVENTION: RANK LIGAND-BINDING POLYPEPTIDES
; FILE REFERENCE: 0226w0310
; CURRENT APPLICATION NUMBER: US/10/467,243
; PRIOR FILING DATE: 2003-08-06
; PRIOR APPLICATION NUMBER: DK PA 2001 00214
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/267,843
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: DK PA 2001 00498
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/278,320
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 401
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-467-243-2

Query Match 100.0%; Score 2085; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 3.1e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLDCDKPPGYLKHCHTAKWTKVCAPCPDHYTDSWHTSDECL 60
DB 22 ETTPPKYLHYDEETSHQLLDCDKPPGYLKHCHTAKWTKVCAPCPDHYTDSWHTSDECL 81
QY 61 YCSPVCKELQYVQKCNTHNRVCECKGRYLEIEFCLKHSRCPGFGVQAGTPERNIV 120
DB 82 YCSPVCKELQYVQKCNTHNRVCECKGRYLEIEFCLKHSRCPGFGVQAGTPERNIV 141
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCVSGVGLLLTQKGNATHDNICSGNSESTQKCGIDVTIL 180
DB 142 CKRCPDGFSSNETSSKAPCRKHTNCVSGVGLLLTQKGNATHDNICSGNSESTQKCGIDVTIL 201
QY 181 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKLWKHQN 240
DB 202 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKLWKHQN 261
QY 241 KAQDIVVKIIQDIDLCEVSRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 262 KAQDIVVKIIQDIDLCEVSRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 321
QY 301 SDQILKLLSLWRINKNGDDTLKGLMHALKHSTYHFFKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SDQILKLLSLWRINKNGDDTLKGLMHALKHSTYHFFKTVTQSLKKTIRFLHSFTMYKLY 381
QY 361 QKLFLEMIGNQVQSVKISCL 380
DB 382 QKLFLEMIGNQVQSVKISCL 401

RESULT 7

US-10-676-358-6
; Sequence 6, Application US/10676358
; Publication No. US20040137074A1
; GENERAL INFORMATION:
; APPLICANT: Nestec SA
; TITLE OF INVENTION: Osteoprotegerin in Milk
; FILE REFERENCE: 88265-6852
; CURRENT APPLICATION NUMBER: US/10/676,358
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: WO 2002 EP 02912
; PRIOR FILING DATE: 2003-03-15
; PRIOR APPLICATION NUMBER: EP 20010108414
; PRIOR FILING DATE: 2001-04-03
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 537
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; OTHER INFORMATION: protein sequence including mature OPG
US-10-676-358-6

Query Match 100.0%; Score 2085; DB 16; Length 537;
Best Local Similarity 100.0%; Pred. No. 4.6e-167;
Matches 380; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLDCDKPPGYLKHCHTAKWTKVCAPCPDHYTDSWHTSDECL 60
DB 158 ETTPPKYLHYDEETSHQLLDCDKPPGYLKHCHTAKWTKVCAPCPDHYTDSWHTSDECL 217
QY 61 YCSPVCKELQYVQKCNTHNRVCECKGRYLEIEFCLKHSRCPGFGVQAGTPERNIV 120
DB 218 YCSPVCKELQYVQKCNTHNRVCECKGRYLEIEFCLKHSRCPGFGVQAGTPERNIV 277
QY 121 CKRCPDGFSSNETSSKAPCRKHTNCVSGVGLLLTQKGNATHDNICSGNSESTQKCGIDVTIL 180

DB 278 CKRCPDGFSSNETSSKAPCRKHTNCVSGVGLLLTQKGNATHDNICSGNSESTQKCGIDVTIL 337
QY 181 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKLWKHQN 240
DB 338 CEEAFFFAVPTKFTPNWLSVLDNLPCTKVNAESVERIKROHSSQEQTFOLLKLWKHQN 397
QY 241 KAQDIVVKIIQDIDLCEVSRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 300
DB 398 KAQDIVVKIIQDIDLCEVSRHIGHANLTFEQLRSLMESLPGKKVGAEDIEKTIKACKP 457
QY 301 SDQILKLLSLWRINKNGDDTLKGLMHALKHSTYHFFKTVTQSLKKTIRFLHSFTMYKLY 360
DB 458 SDQILKLLSLWRINKNGDDTLKGLMHALKHSTYHFFKTVTQSLKKTIRFLHSFTMYKLY 517
QY 361 QKLFLEMIGNQVQSVKISCL 380
DB 518 QKLFLEMIGNQVQSVKISCL 537

RESULT 8

US-09-062-113-4
; Sequence 4, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; TITLE OF INVENTION: the Proteins
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
; FILING DATE: 20-FEB-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000

; TELEFAX: (617) 248-7100
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 380 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; NAME/KEY: Protein
 ; LOCATION: 1..380
 ; OTHER INFORMATION: /note= "(OCIF protein without
 ; OTHER INFORMATION: signal peptide)"
 ; US-09-062-113-4

Query Match 99.7%; Score 2079; DB 9; Length 380;
 Best Local Similarity 99.7%; Pred. No. 9.4e-167;
 Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 Db 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPERTV 120
 Db 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPERTV 120
 QY 121 CKRCPDGFFSNSTSSKAPCKRKHNTCSVFGLLLTQKGNATHDNCNCSNSESTQKCGIDVTL 180
 Db 121 CKRCPDGFFSNSTSSKAPCKRKHNTCSVFGLLLTQKGNATHDNCNCSNSESTQKCGIDVTL 180
 QY 181 CBEAFFRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOQTFQLLKLWKHQN 240
 Db 181 CBEAFFRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOQTFQLLKLWKHQN 240
 QY 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 Db 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 QY 301 SQIILKLLSLWRINKGDQDTLKLGMALHKSHTYHPKVTQSLKKTIRFLHSFTMYKLY 360
 Db 301 SQIILKLLSLWRINKGDQDTLKLGMALHKSHTYHPKVTQSLKKTIRFLHSFTMYKLY 360
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 9

US-10-232-858-4
 ; Sequence 4, Application US/10232858
 ; Publication No. US20030153048A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOTO, Masaaki
 ; APPLICANT: TSUDA, Eisuke
 ; APPLICANT: MOCHIZUKI, Shin'ichi
 ; APPLICANT: YANO, Kazuki
 ; APPLICANT: KOBAYASHI, Fumie
 ; APPLICANT: SHIWA, No. US20030153048A1uyuki
 ; APPLICANT: YASUDA, Hisataka
 ; APPLICANT: NAKAGAWA, No. US20030153048A1uaki
 ; APPLICANT: MORINAGA, Tomonori
 ; APPLICANT: UEDA, Masatsugu
 ; APPLICANT: HIGASHIO, Kanji
 ; TITLE OF INVENTION: No. US20030153048A1el Proteins and Methods for Producing the Prot
 ; FILE REFERENCE: 16991.004
 ; CURRENT APPLICATION NUMBER: US/10/232,858
 ; CURRENT FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: PCT/JP96/00374
 ; PRIOR FILING DATE: 1996-02-20
 ; PRIOR APPLICATION NUMBER: 08/915,004
 ; PRIOR FILING DATE: 1997-08-20
 ; NUMBER OF SEQ ID NOS: 108

; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 380
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-232-858-4

Query Match 99.7%; Score 2079; DB 14; Length 380;
 Best Local Similarity 99.7%; Pred. No. 9.4e-167;
 Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 Db 1 ETPPKYLHYDEETSHQLCDKCPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPERTV 120
 Db 61 YCSPVCKELQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGPGFVGVQAGTPERTV 120
 QY 121 CKRCPDGFFSNSTSSKAPCKRKHNTCSVFGLLLTQKGNATHDNCNCSNSESTQKCGIDVTL 180
 Db 121 CKRCPDGFFSNSTSSKAPCKRKHNTCSVFGLLLTQKGNATHDNCNCSNSESTQKCGIDVTL 180
 QY 181 CBEAFFRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOQTFQLLKLWKHQN 240
 Db 181 CBEAFFRFAVPTKFTPNWLSVLDNLPGTKVNAESVERIKRQHSOQTFQLLKLWKHQN 240
 QY 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 Db 241 KAQDIVKKLIQDIDLCEVSVQRHIGHANLTFEQLRSLMESLPKKVGAEDIEKTIKACP 300
 QY 301 SQIILKLLSLWRINKGDQDTLKLGMALHKSHTYHPKVTQSLKKTIRFLHSFTMYKLY 360
 Db 301 SQIILKLLSLWRINKGDQDTLKLGMALHKSHTYHPKVTQSLKKTIRFLHSFTMYKLY 360
 QY 361 QKLFLEMIGNQVQSVKISCL 380
 Db 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 10

US-10-785-109-4
 ; Sequence 4, Application US/10785109
 ; Publication No. US20040142426A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GOTO, Masaaki
 ; APPLICANT: TSUDA, Eisuke
 ; APPLICANT: MOCHIZUKI, Shin'ichi
 ; APPLICANT: YANO, Kazuki
 ; APPLICANT: KOBAYASHI, Fumie
 ; APPLICANT: SHIWA, Nobuyuki
 ; APPLICANT: YASUDA, Hisataka
 ; APPLICANT: NAKAGAWA, Nobuaki
 ; APPLICANT: MORINAGA, Tomonori
 ; APPLICANT: UEDA, Masatsugu
 ; APPLICANT: HIGASHIO, Kanji
 ; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
 ; FILE REFERENCE: 16991.017
 ; CURRENT APPLICATION NUMBER: US/10/785,109
 ; CURRENT FILING DATE: 2004-02-25
 ; PRIOR APPLICATION NUMBER: US 10/232,858
 ; PRIOR FILING DATE: 2002-09-03
 ; PRIOR APPLICATION NUMBER: US 08/915,004
 ; PRIOR FILING DATE: 1997-08-20
 ; PRIOR APPLICATION NUMBER: PCT/JP96/00374
 ; PRIOR FILING DATE: 1996-02-20
 ; PRIOR APPLICATION NUMBER: JP 207508/1995
 ; PRIOR FILING DATE: 1995-07-21
 ; PRIOR APPLICATION NUMBER: JP 054977/1995
 ; PRIOR FILING DATE: 1995-02-20
 ; NUMBER OF SEQ ID NOS: 108
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4

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; LENGTH: 380
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-109-4
Query Match          99.7%; Score 2079; DB 16; Length 380;
Best Local Similarity 99.7%; Pred. No. 9.4e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSMHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSMHTSDECL 60
QY 61 YCSPVKELQVQKOECHNRTHRVCECKEGRYLEFCLKHSRCPGGVQAGTPERNIV 120
DB 61 YCSPVKELQVQKOECHNRTHRVCECKEGRYLEFCLKHSRCPGGVQAGTPERNIV 120
QY 121 CKRCPDGFNSETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
DB 121 CKRCPDGFNSETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
QY 181 CEEAFFFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHQN 240
DB 181 CEEAFFFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHQN 240
QY 241 KAQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDEIKTIKACP 300
DB 241 KDQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDEIKTIKACP 300
QY 301 SDQILKLLSLWRKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 301 SDQILKLLSLWRKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
QY 361 QKLFLEMIGNQVQSVKISCL 380
DB 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 11
US-10-785-114-4
; Sequence 4, Application US/10785114
; Publication No. US20040143859A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; FILE REFERENCE: 16991.016
; CURRENT APPLICATION NUMBER: US/10785,114
; PRIOR FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004
; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 380
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-785-114-4
Query Match          99.7%; Score 2079; DB 16; Length 380;
Best Local Similarity 99.7%; Pred. No. 9.4e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSMHTSDECL 60
DB 1 ETTPPKYLHYDEETSHQLLCKCPGTYLKQHCCTAKWKTVCAPCPDHYTDSMHTSDECL 60
QY 61 YCSPVKELQVQKOECHNRTHRVCECKEGRYLEFCLKHSRCPGGVQAGTPERNIV 120
DB 61 YCSPVKELQVQKOECHNRTHRVCECKEGRYLEFCLKHSRCPGGVQAGTPERNIV 120
QY 121 CKRCPDGFNSETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
DB 121 CKRCPDGFNSETSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
QY 181 CEEAFFFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHQN 240
DB 181 CEEAFFFAVPTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEOTFOLLKLWKHQN 240
QY 241 KAQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDEIKTIKACP 300
DB 241 KDQDIVKKIIODIDL CENSQVORHIGHANLTPEQLRSLSMESLPGRKVGAEDEIKTIKACP 300
QY 301 SDQILKLLSLWRKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 301 SDQILKLLSLWRKNGDQDTL KGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
QY 361 QKLFLEMIGNQVQSVKISCL 380
DB 361 QKLFLEMIGNQVQSVKISCL 380

RESULT 12
US-09-062-113-106
; Sequence 106, Application US/09062113
; Patent No. US20020051969A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, No. US20020051969A1uyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20020051969A1uaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20020051969A1el Proteins and Methods for Producing
; NUMBER OF SEQUENCES: 108
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Testa, Hurwitz & Thibault
; STREET: 125 High St.
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/062,113
; FILING DATE: 17-APR-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 54977/1995
```

; FILING DATE: 20-FEB-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: JP 207508/1995
; FILING DATE: 21-JUL-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/00374
; FILING DATE: 20-FEB-1996
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/915,004
; FILING DATE: 20-FEB-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: MOORE, Ronda P.
; REGISTRATION NUMBER: 44,244
; REFERENCE/DOCKET NUMBER: FJN-060DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 248-7000
; TELEFAX: (617) 248-7100
; INFORMATION FOR SEQ ID NO: 106:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 391 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-062-113-106

Query Match 99.7%; Score 2079; DB 9; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	60
DB	12	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	71
QY	61	YCSPVCKELQYKQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVGVQAATPERNTV	120
DB	72	YCSPVCKELQYKQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVGVQAATPERNTV	131
QY	121	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	180
DB	132	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	191
QY	181	CBEAFPRFAPVTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	240
DB	192	CBEAFPRFAPVTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	251
QY	241	KQADIVKKLIQDIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	300
DB	252	KQDQDIVKKLIQDIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	311
QY	301	SQIILKLLSLWRIKNGDQDTLKLGMHALKHSKTYHPPKTVTQSLKKTIRFLHSFTMYKLY	360
DB	312	SQIILKLLSLWRIKNGDQDTLKLGMHALKHSKTYHPPKTVTQSLKKTIRFLHSFTMYKLY	371
QY	361	QKLFLEMIGNQVQSVKISCL	380
DB	372	QKLFLEMIGNQVQSVKISCL	391

RESULT 13

US-10-232-858-106
; Sequence 106, Application US/10232858
; Publication No. US20030153048A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, No. US20030153048A1
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu

; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: No. US20030153048A1el Proteins and Methods for Producing the Prote
; FILE REFERENCE: 16991.004
; CURRENT APPLICATION NUMBER: US/10/232,858
; CURRENT FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: 08/915,004
; PRIOR FILING DATE: 1997-08-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-232-858-106

Query Match 99.7%; Score 2079; DB 14; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	1	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	60
DB	12	ETPPKYLHYDEETSHQLLCKDCPPGTYLKQHCTAKWKTVCAPCPDHYTDSWHTSDECL	71
QY	61	YCSPVCKELQYKQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVGVQAATPERNTV	120
DB	72	YCSPVCKELQYKQECNRTHNRVCECKEGRYLIEFCLKHSRCPGPGVGVQAATPERNTV	131
QY	121	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	180
DB	132	CKRCPDGFSSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNCSNBSSTQKCGIDVTL	191
QY	181	CBEAFPRFAPVTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	240
DB	192	CBEAFPRFAPVTKFTPNWLSVLVDNLPGTKVNAESVERIKRQHSSEQTFFQLLKLWKHQ	251
QY	241	KQADIVKKLIQDIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	300
DB	252	KQDQDIVKKLIQDIDLCNSVQRHIGHANLTFEQLRSIMESLPKGVGAEDIEKTIKACP	311
QY	301	SQIILKLLSLWRIKNGDQDTLKLGMHALKHSKTYHPPKTVTQSLKKTIRFLHSFTMYKLY	360
DB	312	SQIILKLLSLWRIKNGDQDTLKLGMHALKHSKTYHPPKTVTQSLKKTIRFLHSFTMYKLY	371
QY	361	QKLFLEMIGNQVQSVKISCL	380
DB	372	QKLFLEMIGNQVQSVKISCL	391

RESULT 14

US-10-785-109-106
; Sequence 106, Application US/10785109
; Publication No. US20040142426A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; CURRENT APPLICATION NUMBER: US/10/785,109
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004

```

; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-109-106

Query Match      99.7%; Score 2079; DB 16; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1  ETPPKVILHYDEETSHQLLCDKCPGGTYLKQHCTAKWKTVCAPCPDHVYTTDSWHTSDECL 60
Db 12  ETPPKVILHYDEETSHQLLCDKCPGGTYLKQHCTAKWKTVCAPCPDHVYTTDSWHTSDECL 71
Qy 61  YCSPVCKELOVYKQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 120
Db 72  YCSPVCKELOVYKQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 131
Qy 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 132  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 191
Qy 181  CEEAFFRPAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSSEOTFOLLKWLKHQN 240
Db 192  CEEAFFRPAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSSEOTFOLLKWLKHQN 251
Qy 241  KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRS LMESLP GKVKVGAEDIEKTIKACKP 300
Db 252  KDQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRS LMESLP GKVKVGAEDIEKTIKACKP 311
Qy 301  SDQILKLLSLWRIKNGDQDTL KGLMHALKSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 312  SDQILKLLSLWRIKNGDQDTL KGLMHALKSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 371
Qy 361  QKLFLEMIGNOVQSVKISCL 380
Db 372  QKLFLEMIGNOVQSVKISCL 391

RESULT 15
US-10-785-114-106
; Sequence 106, Application US/10785114
; Publication No. US20040143859A1
; GENERAL INFORMATION:
; APPLICANT: GOTO, Masaaki
; APPLICANT: TSUDA, Eisuke
; APPLICANT: MOCHIZUKI, Shin'ichi
; APPLICANT: YANO, Kazuki
; APPLICANT: KOBAYASHI, Fumie
; APPLICANT: SHIMA, Nobuyuki
; APPLICANT: YASUDA, Hisataka
; APPLICANT: NAKAGAWA, Nobuaki
; APPLICANT: MORINAGA, Tomonori
; APPLICANT: UEDA, Masatsugu
; APPLICANT: HIGASHIO, Kanji
; TITLE OF INVENTION: Novel Proteins and Methods for Producing the Proteins
; FILE REFERENCE: 16991.016
; CURRENT APPLICATION NUMBER: US/10/785,114
; CURRENT FILING DATE: 2004-02-25
; PRIOR APPLICATION NUMBER: US 10/232,858
; PRIOR FILING DATE: 2002-09-03
; PRIOR APPLICATION NUMBER: US 08/915,004
; PRIOR FILING DATE: 1997-08-20
; PRIOR APPLICATION NUMBER: PCT/JP96/00374
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; PRIOR FILING DATE: 1996-02-20
; PRIOR APPLICATION NUMBER: JP 207508/1995
; PRIOR FILING DATE: 1995-07-21
; PRIOR APPLICATION NUMBER: JP 054977/1995
; PRIOR FILING DATE: 1995-02-20
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 106
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-785-114-106

Query Match      99.7%; Score 2079; DB 16; Length 391;
Best Local Similarity 99.7%; Pred. No. 9.7e-167;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1  ETPPKVILHYDEETSHQLLCDKCPGGTYLKQHCTAKWKTVCAPCPDHVYTTDSWHTSDECL 60
Db 12  ETPPKVILHYDEETSHQLLCDKCPGGTYLKQHCTAKWKTVCAPCPDHVYTTDSWHTSDECL 71
Qy 61  YCSPVCKELOVYKQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 120
Db 72  YCSPVCKELOVYKQECNRTNHRVCECKEGRYLEIEFCLKHRSCPPGFGVVOAGTPERNTV 131
Qy 121  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 180
Db 132  CKRCPDGFPSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI CSGNSESTQKCGIDVTL 191
Qy 181  CEEAFFRPAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSSEOTFOLLKWLKHQN 240
Db 192  CEEAFFRPAVPTKFTPNWLSVLVDNLPCTKVNASVERIKRQHSSEOTFOLLKWLKHQN 251
Qy 241  KAQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRS LMESLP GKVKVGAEDIEKTIKACKP 300
Db 252  KDQDIVKKIIQDIDL CENS VQRHIGHANLTPEQLRS LMESLP GKVKVGAEDIEKTIKACKP 311
Qy 301  SDQILKLLSLWRIKNGDQDTL KGLMHALKSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 312  SDQILKLLSLWRIKNGDQDTL KGLMHALKSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 371
Qy 361  QKLFLEMIGNOVQSVKISCL 380
Db 372  QKLFLEMIGNOVQSVKISCL 391

Search completed: November 15, 2004, 19:04:37
Job time : 147 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 15, 2004, 18:50:46 ; Search time 39 Seconds
(without alignments)
937.497 Million cell updates

Title: US-10-676-358-1

Perfect score: 2085
Sequence: 1 ETFPKYLHYDEETSHQLLC.....QKLFLEMIGNQVQSVKISCL 380

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

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Minimum DB seq length: 0
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Maximum DB seq length: 2000000000

Dist-procedure: $M_{12} = M_{21} = M_{11} + M_{22}$ 08

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:★

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1: pir1:*
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2: pir2:*
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3: pir3:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	336.5	16.1	459	2	I48854	gene murine tumour
2	333.5	16.0	474	2	B38634	tumor necrosis fac
3	330	15.8	461	1	A35356	tumor necrosis fac
4	322.5	15.5	651	2	JC7705	death receptor-6 -
5	284.5	13.6	305	2	A46476	B cell-associated
6	264	12.7	277	2	A60771	B-cell activation
7	239.5	11.5	435	2	I54182	tumor necrosis fac
8	232.5	11.2	348	2	D28623	hypothetical prote
9	232.5	11.2	349	2	D36858	gene G4R protein -
10	229.5	11.0	349	2	D72175	G2R protein - vari
11	225	10.8	325	2	A43692	T2 protein - rabbi
12	219	10.5	326	1	GQVZML	T2 protein - myxom
13	188	9.0	256	2	B32393	T-cell antigen 4-1
14	185.5	8.9	427	1	GQHUN	nerve growth facto
15	185	8.9	461	1	GQRTT1	tumor necrosis fac
16	181.5	8.7	425	1	A26431	nerve growth facto
17	180.5	8.7	314	2	I37383	FAS soluble protei
18	178	8.5	335	2	A40036	apoptosis-mediatin
19	177	8.5	255	2	I38426	lymphocyte activat
20	176	8.4	416	1	JN0006	nerve growth facto
21	176	8.4	454	1	GQMTT1	tumor necrosis fac
22	168	8.1	455	1	GQSTU1	tumor necrosis fac
23	168	8.1	461	2	JC4302	tumor necrosis fac
24	167.5	8.0	271	2	S13783	OX40 antigen precu
25	160.5	7.7	277	2	I37552	OX40 homolog - hum
26	158	7.6	595	2	A42086	CD30 antigen precu
27	149.5	7.2	272	2	I48700	gene ox40 protein
28	146	7.0	324	2	JC2395	Fas antigen precu
29	140	6.7	227	2	A46484	apoptosis-mediatin

30	136.5	6.5	643	2	T25473	hypothetical prote
31	135.5	6.5	2823	2	F87908	protein T22A3.8 [i
32	135.5	6.5	2823	2	T23064	hypothetical prote
33	135.5	6.5	3102	2	T43291	laminin alpha chai
34	135	6.5	1548	2	S34583	serine proteinase
35	134	6.4	398	2	T33383	hypothetical prote
36	133	6.4	1252	2	S36016	cocyst wall protei
37	132.5	6.4	1786	1	MMHUB1	laminin beta-1 cha
38	130	6.2	1790	1	MMFEB1	laminin beta-1 cha
39	129.5	6.2	1369	2	S70713	protein-tyrosine k
40	129.5	6.2	2918	2	A54105	fibrillin-2 precur
41	128.5	6.2	899	2	G02428	subtilisin-like pr
42	128.5	6.2	915	2	JC6148	subtilisin-like pr
43	128	6.1	3712	2	S18553	laminin alpha-1 ch
44	127.5	6.1	2610	2	T20968	hypothetical prote
45	126.5	6.1	1786	1	MMHGB1	laminin beta-1 cha

ALIGNMENTS

RESULT 1
I48854
gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I48854
R/Powell, E.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
Mamm. Genome 5, 726-727, 1994
A/Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
A/Reference number: I48854; MUID:95178848; PMID:7873884
A/Accession: I48854
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-459 <RES>
A/Cross-references: UNIPROT:Q63227; EMBL:X76401; NID:G433830; PID:G433830
C/Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolog
F;151-188/Domain: NGF receptor repeat homology <NGF>

Query Match	16.1%;	Score 336.5;	DB 2;	Length 459;
Best Local Similarity	35.7%;	Pred. No. 1.7e-15;		
Matches 74;	Conservative 23;	Mismatches 85;	Indels 25;	Gaps 6;

QY	9	HYDEETSHQLLCDKCPPTYLKQCTAKWTKVACPCPDHYTDSWITSDECLYCSVPCKE	68
Db	31	Y YDRKA--QMCAKCPGQYVKHFCNKTSDTVACDCEASMYTQVWQFRTCLSCSSCSST	88
QY	69	LQYVQECNRTHNVACEKREGLYLEIF-----CLKHRS CPBGQVVOAGTPEHNWVC	121
Db	89	DOVETRAC TKQONRVCAEAGRYCALKTHSGRCQCMRLSKCGPFGFVASSRAPNGNVLIC	148
QY	122	KRCPDGFFSNETSKAPCRKHTNCVSFGLLLTKQGNATHDNICSGNSESTKCGIDVILIC	181
Db	149	KACAPGFSDTSTSDVCRPHRICSLAI-----PGNASTDAVCA--PESPTLSAIPRTL-	201
QY	182	EEAFRRFAVPTKTFPNWLSVLVDNLPG	208
Db	202	---YVSOPETSESOP-----tlnofbg	219

RESULT 2
B38634

tumor necrosis factor receptor type 2 precursor - mouse
 C;Species: Mus musculus [house mouse]
 C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #tex
 C;Accession: B38634; A40254; S54846
 R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; R
 Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A;Title: Cloning and expression of cDNAs for two disti
 A;Reference number: A36534; MUID:51187805; PMID:1849278
 A;Accession: B38634
 A;Molecule type: mRNA
 A;Residues: 1-474 <1ev>

A;Cross-references: UNIPROT:P25119; GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk
 Mol. Cell. Biol. 11, 3020-3026, 1991
 A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for
 A;Reference number: A40254; MUID:91246168; PMID:1645445
 A;Accession: A40254
 A;Molecule type: mRNA
 A;Residues: 1-474 <GO>
 A;Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R;Kisnerghis, M.; Fellows, R.; Feldmann, M.; Chernajovskiy, Y.
 submitted to the EMBL Data Library, May 1995
 A;Description: Characterization of the promoter region of the murine p75-TNFR receptor.
 A;Reference number: S54816
 A;Accession: S54816
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-22 <KIS>
 A;Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C;Keywords: cytokine receptor; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F;40-77/Domain: NGF receptor repeat homology <NG1>
 F;79-120/Domain: NGF receptor repeat homology <NG2>
 F;166-203/Domain: NGF receptor repeat homology <NG4>
 Query Match 16.0%; Score 333.5; DB 2; Length 474;
 Best Local Similarity 35.7%; Pred. No. 2.8e-15;
 Matches 74; Conservative 23; Mismatches 85; Indels 25; Gaps 6;
 QY 9 HYDEETSHOLLCDKCPGGYLYKHCHTAKWTCAPCPDHYHYSWHTSDECLYCSPVCKE 68
 DB 46 YDRA--QMCACKPPGGYVYKHFNKTSITVCACEASWYQVWVNFRTCLSSSCTT 103
 QY 69 LQYVQECNRTHNRVCEKEGRYLEIF-----CLKHRSPPGFGVVQAGTPERNVVC 121
 DB 104 DQVEIRACTQKNRVACACEAGRYCALKTHSGSCRCQMLSKGCPGFGVASSRAPNGVLC 163
 QY 122 KCPDGGFSNETSSKAPCKRHNCVFGILLQKGNATHDNCSGNSESTQCGIDVTLC 181
 DB 164 KACAPGTFSDTTSSTDVCSPHRCISLAI-----PGNASTDAVCA--PESFTLSAIPRTU- 216
 QY 182 BEAFRFAPVPTFTFNWLSVLVDNLPG 208
 DB 217 ---YVSQPEPTRSQP-----LDQEPG 234
 RESULT 3
 A35356
 tumor necrosis factor receptor 2 precursor [validated] - human
 N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2
 C;Species: Homo sapiens (man)
 C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 09-Jul-2004
 C;Accession: A35356; A48416; A36007; A23666; B35010; I38094
 R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K
 Science 248, 1019-1023, 1990
 A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and
 A;Reference number: A35356; MUID:90260639; PMID:2160731
 A;Accession: A35356
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-461 <SWI>
 A;Cross-references: UNIPROT:P20333; GB:M32315; NID:g189185; PIDN:AAA5929.1; PID:g189186
 R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A;Reference number: A36475; MUID:91045991; PMID:2172983
 A;Accession: A36475
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-195, 'R', 197-461 <KOH>
 A;Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990
 A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,
 A;Reference number: A48416; MUID:91370690; PMID:1966549
 A;Accession: A48416
 A;Status: preliminary
 A;Molecule type: mRNA; protein
 A;Residues: 23-461 <DEM>
 A;Cross-references: GB:S63368; NID:g235648; PIDN:AA19824.1; PID:g235649
 R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra
 A;Reference number: A36007; MUID:90349572; PMID:2166946
 A;Accession: A36007
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>
 A;Cross-references: GB:M35857; NID:g339751; PIDN:AA63262.1; PID:g339752
 R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.
 J. Biol. Chem. 265, 20131-20138, 1990
 A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A;Reference number: A23666; MUID:91056048; PMID:2173696
 A;Accession: A23666
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 23-40;65-69;136-141;300-306 <LOE>
 R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A;Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A;Reference number: A35010; MUID:90110215; PMID:2153136
 A;Accession: B35010
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 27-31 <ENG>
 R;Kuhnert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A;Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A;Reference number: I38094; MUID:95121934; PMID:7821811
 A;Accession: I38094
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-37 <RES>
 A;Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 C;Genetics:
 A;Gene: GDB:TNFR2
 A;Cross-references: GDB:125914; OMIM:191191
 A;Map position: 1p36.2-1p36.2
 A;Introns: 26/3
 A;Note: the list of introns is incomplete
 C;Superfamily: tumor necrosis factor receptor type 2 (TNFR2); NGF receptor repeat homolo
 C;Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F;1-22/Domain: signal sequence #status predicted <SIG>
 F;23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F;40-76/Domain: NGF receptor repeat homology <NG1>
 F;78-119/Domain: NGF receptor repeat homology <NG2>
 F;120-162/Domain: NGF receptor repeat homology <NG3>
 F;164-201/Domain: NGF receptor repeat homology <NG4>
 F;262-279/Domain: transmembrane #status predicted <TMN>
 F;280-461/Domain: intracellular #status predicted <INT>
 F;171.193/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 15.8%; Score 330; DB 1; Length 461;
 Best Local Similarity 39.8%; Pred. No. 4.7e-15;
 Matches 66; Conservative 16; Mismatches 72; Indels 12; Gaps 3;
 QY 9 HYDEETSHOLLCDKCPGGYLYKHCHTAKWTCAPCPDHYHYSWHTSDECLYCSPVCKE 68
 DB 45 YDQ--TAQMCCSKSPGGHAKVFCRTSDTVCDSCESTYTQLNWNVPECLSGSRCS 102
 QY 69 LQYVQECNRTHNRVCEKEGRYLEI-----BFLKLRSCPPGFGVVQAGTPERNVVC 122
 DB 103 DQVEIRACTQKNRITCTCRPGWYCALSKQEGCLCAPLRKCRPGFGVAREGTETSDVVC 162

QY 123 RCPDGFPSNETSSKAPCRKHTNCVSFGLLLTQKGNATHDNCNS 168
Db 163 PCAPGTFSTTSSTDCRPHQICNVVAI ---PGNASMDAVCTSTS 204

RESULT 4

JC7705
 death receptor-6 - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Jul-2004
 C:Accession: JC7705
 R:Bridgham, J.T.; Bohe, J.; Goetz, F.W.; Johnson, A.L.
 Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001
 A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.
 A:Reference number: JC7705; PMID:21308433; PMID:11414598
 A:Accession: JC7705
 A:Molecule type: mRNA
 A:Residues: 1-651 <BRI>
 A:Cross-references: UNIPROT:Q98SM6; GB:AF349908
 C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs
 C:resia, activates a cell death and/or survival signaling cascade.

C;Genetics:
A;Gene: dr-6
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous domain
C;Keywords: ovary
F;1-21/Domain: signal sequence #status predicted <SIG>
F;52-136/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;332-350/Domain: transmembrane #status predicted <TM>
F;410-475/Domain: death domain #status predicted <DED>
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match	15.5%;	Score	322.5;	DB 2;	Length	651;			
Best Local Similarity	31.8%;	Pred. No.	2.2e-14;						
Matches	69;	Conservative	36;	Mismatches	105;	Indels	7;	Gaps	3
QY	6	KYLHYDEBTSHOLLCDKCPGTYLKHQHTAKWKTVCAPCDHYHYDSMHTSDECLYCSFV	65						
Db	38	KYLHLDRATNOELICDKCPAGTYVSKHTKSTLRCSPCPGDTFFKHENGHERCHPCRP	97						
QY	66	KLELYVYKQECNRTHNRVCECKEGRYLBIEFLKHSRCPGFGVVOAGTTPRNTVCKRCP	125						
Db	98	CELFMIKXTHCTALTDRRECTCLSGTFQINDTCVPYTCVGVGVRKKGKTETEDVCKPCL	157						
QY	126	DGFFSNETSSKAPCRKHTNCSVFGLLTQGNATHDNICSGNSE--STQKCGIDVTLCGE	183						
Db	158	RGTFSDVPSSVMKCKTYDCRGKNNVWPGTKESDNVCKSPASLPNTSLTSSDAQDGE	217						
QY	184	AFRFAVPTKFTPNWLSVLVDNL---PGTKVNABSE	217						
Db	218	TY--EAPPTALPKGLNSSFDFLSSSPAPRVNSGTAE	252						

RESULT 5

A46476
 B cell-associated surface molecule CD40, long splice form - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 18-Jun-1993 #sequence
 C;Accession: A46476; A46515
 R;Torres, R.M.; Clark, E.A.
 J. Immunol. 148, 620-626, 1992
 A;Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40
 A;Reference number: A46476; MUID:92105763; PMID:1370315
 A;Accession: A46476
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-305 <TOR>
 A;Cross-references: UNIPROT:P27512; GB:M83312; NID:G1553058
 A;Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P.75207)
 A;Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
 R;Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.
 J. Immunol. 149, 3921-3926, 1992
 A;Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
 A;Reference number: A46515; MUID:93094586; PMID:1281194

A;Accession: A46515
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: nucleic acid
A;Accession: 1-287,'LV','GRI'
A;Cross-references: GR<M3312>
A;Experimental source: BALB/C, liver
A;Note: sequence extracted from NCBI backbone (NCBI:120357)
C;Comment: For an alternative splice form, see PR:A46515.
C;Comment: For an alternative splice form, see PR:A46476.
C;Superfamily: CD27 antigen; NGF receptor repeat homology
C;Keywords: alternative splicing; transmembrane protein
F;1:05-144/Domain: NGF receptor repeat homology <NGF>

[illegible]

RESULT 6

A60771
 B-cell activation protein CD40 precursor - human
 B-Cell alternate names: B-cell surface antigen Bp50
 C-Species: Homo sapiens (man)
 C-Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C-Accession: S04460; A60771
 R:Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMO J. 8, 1403-1410, 1989
 A>Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A:Reference number: S04460; MUID:89356608; PMID:2475341
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <STA>
 A:Cross-References: UNIPROT:P25942; EMBL:X60592; NID:G29850; PIDN:CAA43045.1; PID:G29851
 R:Brasch-Andersen, S.; Paulie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A>Title: Biochemical characteristics and partial amino acid sequence of the receptor-like
 A:Reference number: A60771; MUID:89093941; PMID:2463309
 A:Accession: A60771
 A:Molecule type: protein
 A:Residues: 21-50 <BRA>
 A:Experimental source: Burkitt lymphoma cell line Raji
 C:Genetics:
 A:Gene: GDB:CD40
 A:Cross-References: GDB:215268; OMIM:109535
 A:Map position: 20q12-20q13.2
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F1-20/Domain: signal sequence #status predicted <SIG>
 F121-277/Product: B-cell activation protein CD40 #status experimental <MAT>

C:Genetics:

A:Gene: G4R
 C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
 F:32-66/Domain: NGF receptor repeat homology <NGF>
 F:68-109/Domain: NGF receptor repeat homology <NG2>
 F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 11.2%; Score 232.5; DB 2; Length 349;
 Best Local Similarity 23.6%; Pred. No. 1.4e-08;
 Matches 89; Conservative 47; Mismatches 158; Indels 83; Gaps 14;

QY 4 PPKYLHYDEE-TSHQLLCKPCPGTYLKQCHTAKWTVCAPCDPHYVYDTSWHTSDCLYC 62
 DB 27 PPKGCKKDEYKRNHLCCLSCPGTYASRLCDSTNTQCTPCGSGTFTSRNNHLPACLSC 86
 QY 63 SPVCKELQYVKQECNRTHNVCKEGRYLEI-----EFLKHSRCPGPGVWQAGTPE 116
 DB 87 NGRCSNQVETRSCNTHNRICECPGYCLLKSGSGCKACVQTKGIGYG-VSGHTSV 145
 QY 117 RNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI-----SGNSEST 171
 DB 146 GDVICSFCGFGTYSHTVSSADKCEPVNNTFNIDVETILYPVNDTSCRTTITGLSESI 205
 QY 172 QKCGIDVTLL-----CEAFPRFAVPTKFTPNWLSVLVDNLPQTKVNAESVRIKQHSQ 227
 DB 206 LTSBELATITMNHDTDCNPVF-----RE 225
 QY 228 QTFOLLK-----LWKHONKAQDIVKIIQDIDLCEMSVQRHIGHANLTFEOLRLMESL 281
 DB 226 EYFSLVKVATSGFFTGENRYQNLK-----VCTLNFBIKCNKNGSSFKQJTKAKND- 277
 QY 282 PGKVGAEIDIEKTIKA-CKPSDQILKLLSLWRINKNGDQDILKGLMHALKHKSXTYHFP--- 337
 DB 278 DGMMSHSETV--TLAGDCLSSVDIYILYNTNAQDYETDISYRVGNVLDLDDDS-HMPGSC 334
 QY 338 ---KTVTQSLUKTIRFL 351
 DB 335 NIHKPTINS--KPTRFL 349

RESULT 10

D72175
 G2R protein - variola minor virus (strain Garcia-1966)
 C:Species: variola minor virus
 C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 09-Jul-2004
 C:Accession: D72175
 R:Shchelkunov, S.N.; Totmenin, A.V.; Gutorov, V.V.; Safronov, P.F.; Massung, R.F.; Lopar
 submitted to GenBank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: D72175
 A:Molecule type: DNA
 A:Residues: 1-349 <SHC>
 A:Cross-references: UNIPROT:P34015; GB:X16780; NID:g5830555; PIDN:CAB54798.1; PID:g58307
 A:Experimental source: strain Garcia-1966
 C:Genetics:
 A:Gene: G2R
 C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 11.0%; Score 229.5; DB 2; Length 349;
 Best Local Similarity 23.6%; Pred. No. 2.3e-08;
 Matches 89; Conservative 46; Mismatches 159; Indels 83; Gaps 14;

QY 4 PPKYLHYDEE-TSHQLLCKPCPGTYLKQCHTAKWTVCAPCDPHYVYDTSWHTSDCLYC 62
 DB 27 PPKGCKKDEYKRNHLCCLSCPGTYASRLCDSTNTQCTPCGSGTFTSRNNHLPACLSC 86
 QY 63 SPVCKELQYVKQECNRTHNVCKEGRYLEI-----EFLKHSRCPGPGVWQAGTPE 116
 DB 87 NGRCSNQVETRSCNTHNRICECPGYCLLKSGSGCKACVQTKGIGYG-VSGHTSV 145
 QY 117 RNTVCKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQGNATHDNI-----SGNSEST 171

DB 146 GDVICSFCGFGTYSHTVSSADKCEPVNNTFNIDVETILYPVNDTSCRTTITGLSESI 205
 QY 172 QKCGIDVTLL-----CEAFPRFAVPTKFTPNWLSVLVDNLPQTKVNAESVRIKQHSQ 227
 DB 206 LTSBELATITMNHDTDCNPVF-----RE 225
 QY 228 QTFOLLK-----LWKHONKAQDIVKIIQDIDLCEMSVQRHIGHANLTFEOLRLMESL 281
 DB 226 EYFSLVKVATSGFFTGENRYQNLK-----VCTLNFBIKCNKNGSSFKQJTKAKND- 277
 QY 282 PGKVGAEIDIEKTIKA-CKPSDQILKLLSLWRINKNGDQDILKGLMHALKHKSXTYHFP--- 337
 DB 278 DGMMSHSETV--TLAGDCLSSVDIYILYNTNAQDYETDISYRVGNVLDLDDDS-HMPGSC 334
 QY 338 ---KTVTQSLUKTIRFL 351
 DB 335 DIHKLTINS--KPTRFL 349

RESULT 11

B43692
 T2 protein - rabbit fibroma virus
 C:Species: rabbit fibroma virus, Shope fibroma virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C:Accession: B43692
 R:Upton, C.; DeLange, A.M.; McFadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
 A:Reference number: A43692; MUID:87321103; PMID:2820128
 A:Accession: B43692
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-325 <UPT>
 A:Cross-references: UNIPROT:P25943; GB:M17433
 C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
 F:64-105/Domain: NGF receptor repeat homology <NG2>
 F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 10.8%; Score 225; DB 2; Length 325;
 Best Local Similarity 30.9%; Pred. No. 4.3e-08;
 Matches 55; Conservative 22; Mismatches 89; Indels 12; Gaps 4;

QY 18 LLCDKCPGCTYLKQCHTAKWTVCAPCDPHYVYDTSWHTSDCLYCSPVCKELQYVKQECN 77
 DB 38 LCCASCHPGFYASRLCGPSNTVCSPECDGTFTASTNHAPACVSCRGCTGHLSESPCD 97
 QY 78 RTHNRVCECKEGRYLEI-----FCLKHSRCPGPGVWQAGTPERNTVCKRCPDGFSSN 131
 DB 98 RTHDRVCNCTGNYCLLKQNGCRICAPQTKCPAGYG-VSGHTRAGDTLCEKCPHTYSD 156
 QY 132 ETSSKAPCRKHTNCSVFGLLLTQGNATHDNI-----CEBAF 185
 DB 157 SLSPTRCGTSFNYSVGNL-YPVNETSCTTAGHNEVIKTEFTVLNTYDTPV 213

RESULT 12

GQVZML

T2 protein - myxoma virus (strain Lausanne)
 C:Species: myxoma virus
 C:Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change 09-Jul-2004
 C:Accession: A40566
 R:Upton, C.; Macen, J.L.; Schreiber, M.; McFadden, G.
 Virology 184, 370-382, 1991
 A:Title: Myxoma virus expresses a secreted protein with homology to the tumor necrosis fa
 A:Reference number: A40566; MUID:91335768; PMID:1651597
 A:Accession: A40566
 A:Molecule type: DNA
 A:Residues: 1-326 <UPT>
 A:Cross-references: UNIPROT:P29825; GB:M95181; GB:M37976; NID:g332309; PIDN:AAA46632.1; I
 C:Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
 C:Keywords: glycoprotein
 F:64-105/Domain: NGF receptor repeat homology <NG2>

F:106-147/Domain: NGF receptor repeat homology <NG3>
F:66,181,205,238/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 10.5%; Score 219; DB 1; Length 326;
Best Local Similarity 30.6%; Pred. No. 1.1e-07;
Matches 55; Conservative 24; Mismatches 85; Indels 16; Gaps 6;
QY 18 L L C D K P P G Y L K Q H C T A K W T V C A P C P D H Y T D S W H T S D B C L Y C S P V C K E L Q V V K Q B C N 77
Db 38 L C C T S C P P G S Y A S L C G P G S D T V C P K N E T F T A S T W H A P A C V S C R G C T G H L S E S Q S C D 97
QY 78 R T H N V C E C K E G R Y L E Y E - - - - - F C L K H R S C P P G F V V Q A G T P E R N T V C K R C P D G F F S N 131
Db 98 K T R D R V C D S A G N Y C L L K G Q G C R I C A P K T C P A G Y G - V S G H T R T G D V L C T K C P R Y T Y S D 156
QY 132 E T S K A P C R K H T N - C S V - F G L L L T Q K N A T H N I C S G N S E S T Q K G I D V I L - - - - - C E A F 185
Db 157 A V S S T E T C T S S F N Y I S V E F N L Y P V - - - - - N D T S C T T T A G E N V V K T S E F S V T L N H T D C D P V F 213
RESULT 13
B32393
T-cell antigen 4-1BB precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C:Accession: B32393; I48879
P:Kwon, B.S.; Weissman, S.M.
Proc. Natl. Acad. Sci. U.S.A. 86, 1963-1967, 1989
A:Title: cDNA sequence of two inducible T-cell genes.
A:Reference number: A32393; MUID:89184547; PMID:2784565
A:Accession: B32393
A:Molecule type: mRNA
A:Residues: 1-256 <KWO>
A:Cross-references: UNIPROT:P20334; GB:J04492; NID:g201121; PIDN:AAA40167.1; PID:g201122
R:Kwon, B.S.; Kozak, C.A.; Kim, K.K.; Picard, R.T.
J. Immunol. 152, 2256-2262, 1994
A:Title: Genomic Organization and Chromosomal Localization of the T-Cell Antigen 4-1BB.
A:Reference number: I48879; MUID:94179805; PMID:8133039
A:Accession: I48879
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-256 <RES>
A:Cross-references: EMBL:U02567; NID:g1117783; PIDN:AAA93113.1; PID:g409178
C:Genetics:
A:Introns: 35/1; 69/1; 115/1; 138/2; 156/3; 181/1; 225/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-256/Product: 4-1BB protein #status predicted <MAT>
Query Match 9.0%; Score 188; DB 2; Length 256;
Best Local Similarity 32.2%; Pred. No. 1.1e-05;
Matches 47; Conservative 18; Mismatches 65; Indels 16; Gaps 6;
QY 20 C D K C P P G Y L K Q H C T A K W T V C A P C P D H Y T D S W H T S D B C L Y C S P V C K E L Q V V K Q E C N R T 79
Db 28 C D N C Q P G T F C R - - - - - K Y N P V C S C P P S T F S - S I G Q P N C N I C R - V C A G Y P R F K F C S S T 80
QY 80 H N R V C E C K E G R Y L E I E F C L K - H R S C P P G F V V Q A G T P E R N T V C K R C P D G F F S N E T S S K A P 138
Db 81 H N A E C E C I E G F H C L G P Q C T R C E K D C R P G Q E L T K Q G - - - - - C K T C S L G T F - N D Q N G T G V 132
QY 139 C R K H N C S V F G L L L T Q K N A T H N I C 164
Db 133 C R P W N C S L D G R S V L K T G T E K D V V C 158
RESULT 14
GQHUN
nerve growth factor receptor precursor, low affinity [validated] - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004

C:Accession: A25218; A60204; S21689; I57638
R:Johnson, D.; Laranhan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.,
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725; PMID:3022937
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <JOH>
A:Cross-references: UNIPROT:P08138; GB:M14764; NID:g189204; PIDN:AA859544.1; PID:g189205
R:Marano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor.
A:Reference number: A60204; MUID:87085574; PMID:3025363
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31, 'T', 33-42, 'T', 45-46, 'T', 50-51, 'X', 54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: this sequence has been corrected by a note added in proof to follow the nucleotide
R:Vissavajhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor rec
A:Reference number: S21689; MUID:92198017; PMID:1372492
A:Accession: S21689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patil, N.; Chao, M.
Mol. Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
A:Reference number: I57638; MUID:89096903; PMID:2850481
A:Accession: I57638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AAA36363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates w
C:Comment: This receptor undergoes both N- and O-linked glycosylation.
C:Genetics:
A:Gene: GDNF-NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>
F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Region: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TRM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted
Query Match 8.9%; Score 185.5; DB 1; Length 427;
Best Local Similarity 33.1%; Pred. No. 2.8e-05;
Matches 48; Conservative 18; Mismatches 62; Indels 17; Gaps 6;
QY 7 Y L H Y D E E T S H Q L L C D K C P P G Y L K Q H C T A K W T V C A P C P D H Y - Y T D S W H T S D B C L Y C S P V 65
Db 37 Y T H S G E - - - - - C C K A C N L G E G V A Q P C G A N - Q T V C E P C L D S V T F S D V V S A T E P C K F C T E - 88
QY 66 C K E L Q V V K Q E C N R T H N R V C E C K E G R Y L E - - - - - I E F C L K H R S C P P G F V V Q A G T P E R N T V 120
Db 89 C V G L Q S M S A P C V E A D D A V C R C A Y G Y Q D E T T G R C E A C - - - - - R V C E A G S G L V F S C D K Q N I V 145
QY 121 C K R C P D G F F S N E T S S K A P C R K H T N C 145
Db 146 C E E C P D G T Y S D E A N H V D P C L P C T V C 170

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RESULT 15
GQRTT1
N:Contains: tumor necrosis factor receptor 1 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Jun-1992 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C:Accession: B36555
R:Himmler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.;
DNA Cell Biol. 9, 705-715, 1990
A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto
A:Reference number: A36555; MUID:91090841; PMID:11702293
A:Accession: B36555
A:Molecule type: mRNA
A:Residues: 1-461 <HIM>
A:Cross-references: UNIPROT:P22934; GB:M61122; NID:g207361; PID:AAA42256.1; PID:g207362
C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo
C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>
F:30-211/Domain: extracellular #status predicted <EXT>
F:44-82/Domain: tumor necrosis factor binding protein #status predicted <TBP>
F:84-126/Domain: NGF receptor repeat homology <NG1>
F:127-167/Domain: NGF receptor repeat homology <NG3>
F:168-204/Domain: NGF receptor repeat homology <NG4>
F:212-234/Domain: transmembrane #status predicted <MEM>
F:235-461/Domain: intracellular #status predicted <INT>
F:54,151,201/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      8.9%; Score 185; DB 1; Length 461;
Best Local Similarity 20.9%; Pred. No. 3.3e-05;
Matches 89; Conservative 47; Mismatches 116; Indels 174; Gaps 21;

QY      6 KYLHYDEETSHQLLCKPPTGYLKQHTAK-WKTVCAPCPDHYTDSWHTSDECLYCSP 64
Db      |||  : : : |||  : : : |||  : : : |||  : : : |||  : : : |||
48 KYAH---PKNNSICTCKKHGTYLVSDCPSPGQGTVEVCVCKGFTTASQNHVRQCLSKT 104

QY      65 VCKELQVVK-QECNRTHNRYCEKKG---RYL-EIEF-CLKHRSCTPGF-GVVQAGTPE 117
Db      |||  : : : |||  : : : |||  : : : |||  : : : |||  : : : |||
105 CRKEMEQVELSPCKADMDTVCGCKKQFQRYLSETHFQCV---DCSPCFNGTIVTPECKE 161

QY      118 -NTVCKKCPDGF--SNETSskaprkhtncsvfgllltokgnathdn----- 162
Db      |||  : : : |||  : : : |||  : : : |||  : : : |||  : : : |||
162 QNTVC-NCHAGFTLSGNECTPCSHCKKNQEC--MKLCPPVANVTNPQDSGTAVLLPLVI 218

QY      163 -----ICSGNSESTQ-----K 173
Db      |||  : : : |||  : : : |||  : : : |||  : : : |||  : : : |||
219 FLGLCLLFFICISLLCRYPQWRPRVYSIIICRDSAPKVEGEGIVTKPLTPASIPAFSPN 278

QY      174 CGIDVTLCBAAPRFAVPTKFTP-----NW----- 198
Db      |||  : : : |||  : : : |||  : : : |||  : : : |||  : : : |||
279 PGFNPTLGFTTFRFSHPVSSITPISPVFGPSNWHNFVPVREVVTQGDPLLYGSLNPV 338

QY      199 -----LSYLDNLFPTK-----VNABSVRIKQ 222
Db      |||  : : : |||  : : : |||  : : : |||  : : : |||  : : : |||
339 PIPAPVRKWDVVAAQFQRLDTADPAMLYAVDVGVPPTWKKEFRLGLSEHEIERLELQ 398

QY      223 HSS--QEQTFFLLKLWKHKQKQ-----DIVKTIQIDIL--CENSVORHIGHANLTFEOL 274
Db      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
399 NGRCLREAHYSMLEAWRRRTPRHEATLDVVGVLCDMLRGC-----LENI 444

QY      275 RSLMES 280
Db      | : |
445 RETLES 450
```

Search completed: November 15, 2004, 19:01:13
Job time : 40 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 15, 2004, 18:38:30 ; Search time 192 Seconds
(without alignments)
1138.762 Million cell updates/sec

Title: US-10-676-358-1

Perfect score: 2085

Sequence: 1 ETFFPKYLHYDEBTSHQLLC.....QKLFLEMIGNQVQSVKISCL 380

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Uniprot_02.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2079	99.7	401	1	TL1B HUMAN
2	1834	88.0	401	2	O6P1I2
3	1834	88.0	401	2	AAH49782
4	1828	87.7	401	1	TL1B RAT
5	1820	87.3	401	1	TL1B MOUSE
6	1028.5	49.3	387	2	O6GLN3
7	525	25.2	146	2	Q7ZZY4
8	450	21.6	186	2	Q7ZZY5
9	440.5	21.1	300	1	TR6B HUMAN
10	411.5	19.7	302	2	O9PU50
11	380.5	18.2	285	2	Q90W71
12	372.5	17.9	285	2	Q90Y56
13	365	17.5	286	2	Q6NM61
14	365	17.5	286	2	AAH67712
15	337	16.2	268	2	O6YI29
16	337	16.2	268	2	AAH72434
17	336.5	16.1	459	2	O62327
18	333.5	16.0	474	1	TR1B MOUSE
19	333.5	16.0	474	2	BAB23533
20	333.5	16.0	474	2	BAB23610
21	330	15.8	461	1	TR1B HUMAN
22	328	15.7	482	2	O88734
23	322.5	15.5	433	2	O91ZM6
24	322.5	15.5	461	2	O6VAU8
25	322.5	15.5	461	2	AAQ22350
26	322.5	15.5	474	2	O80WY6
27	322.5	15.5	651	2	Q9ASM6
28	302.5	14.5	655	1	TR21 HUMAN
29	302.5	14.5	655	2	AAE36088
30	298	14.3	483	2	O800K7
31	297	14.2	457	2	Q81VS6

RESULT 1

32	297	14.2	457	2	AAH11844	Aah11844 homo sapi
33	293	14.1	655	1	TR21 MOUSE	Q9epus mus musculu
34	293	14.1	655	2	BAC31664	Bac31664 mus muscu
35	284.5	13.6	289	1	TNR5 MOUSE	P27512 mus musculu
36	284.5	13.6	289	2	O8K2X6	O8k2x6 mus musculu
37	284.5	13.6	289	2	BAC40978	Bac40978 mus muscu
38	279.5	13.4	467	2	O800I0	Q800i0 gallus gall
39	270	12.9	169	2	O9JKE0	Q9jke0 rattus norv
40	267	12.8	278	2	O8SQ34	Q8sq34 sus scrofa
41	267	12.8	462	2	O805B0	Q805b0 gallus gall
42	265	12.7	276	2	O9DDD2	Q9ddd2 gallus gall
43	264	12.7	223	2	O86VK5	O86vk5 homo sapien
44	264	12.7	277	1	TNR5 HUMAN	P25942 homo sapien
45	257	12.3	318	2	Q7T2H3	Q7t2h3 oncorhynchu

ALIGNMENTS

ID TL1B HUMAN STANDARD; PRT; 401 AA.

AC O00300; O60236; Q9UHP4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 11B precursor

DE (osteoprotegerin) (osteoclastogenesis inhibitory factor).

GN Name=TNFRSF11B; Synonyms=OPG, OCIF;

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=97262071; PubMed=9108485;

RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,

RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,

RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,

RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,

RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,

RA Suggs S., Boyle W.J.;

RT "Osteoprotegerin: a novel secreted protein involved in the regulation

RT of bone density.";

RL Cell 89:309-319(1997).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Lung cancer;

RX MEDLINE=98151033; PubMed=9492069;

RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,

RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,

RA Tsuda E., Morinaga T., Higashio K.;

RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and

RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits

RL osteoclastogenesis in vitro.";

RL Endocrinology 139:1329-1337(1998).

RN [3]

RP SEQUENCE FROM N.A., AND VARIANT ASN-3.

RC TISSUE=Placenta;

RX MEDLINE=98351569; PubMed=9688283;

RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;

RT "Cloning and characterization of the gene encoding human

RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";

RL Eur. J. Biochem. 254:685-691(1998).

RN [4]

RP SEQUENCE FROM N.A., AND VARIANTS ASN-3 AND MET-104.

RA Livingston R.J., Rieder M.J., Chung M.-W., Ritchie T.K., Olson A.N.,

RA Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D., Schackwitz W.S.,

RA Sherwood J.K., Sherwood A.M., Leithausen B.J., Nickerson D.A.;

RT "NIHES-SNPs, environmental genome project, NIHES ES15478, Department

RT of Genome Sciences, Seattle, WA (URL: <http://egp.gs.washington.edu>).";

RL Submitted (NOV-2003) to the EMBL/Genbank/DBJ databases.

[5]
SEQUENCE FROM N.A., AND VARIANT ASN-3.
RT TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Baha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[6]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159; DOI=10.1006/hbrc.1998.8443;
RA Tomoyasu A., Goto M., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RL Biochem. Biophys. Res. Commun. 245:382-387 (1998).
[7]
RN SEQUENCE OF 22-36.
RP Zhang Z., Henzel W.;
RA "Signal peptide prediction based on analysis of experimentally
RT verified cleavage sites.";
RL Submitted (JUN-2004) to Swiss-Prot.
[8]
RN SEQUENCE OF 22-393 FROM N.A.
RP He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RA "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL Acta Biochim. Biophys. Sin. 31:680-684 (1999).
[9]
RN SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977; DOI=10.1006/hbrc.1997.6603;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 234:137-142 (1997).
[10]
RN TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 273:14363-14367 (1998).
[11]
RN CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yamaguchi K., Kinoshita M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor.";
RL J. Biol. Chem. 273:5117-5123 (1998).
[12]
RN REVIEW.
RX MEDLINE=2135914; PubMed=11505389;
RX DOI=10.1002/1097-0142(20010801)92:3<450::AID-CNCR1344>3.0.CO;2-D;
RA Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases.";
RL Cancer 92:460-470 (2001).
[13]
RN VARIANT JPD ASP-182 DEL.
RP PubMed=12189164;
RX Cundy T., Hegde M., Naot D., Chong B., King A., Wallace R., Mulley J.,
RA Love D.R., Seidel J., Pawlner M., Barovich T., Callon K.E., Grey A.B.,
RA Reid I.R., Middleton-Hardie C.A., Cornish J.;
RT "A mutation in the gene TNFRSF11B encoding osteoprotegerin causes an
RT idiopathic hyperphosphatasia phenotype.";
RL Hum. Mol. Genet. 11:2119-2127 (2002).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy
CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and lung.
CC muscle. Highly expressed in fetal kidney, liver and lung.
CC -!- INDUCTION: Up-regulated by increasing calcium-concentration in the
CC medium and estrogens. Down-regulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains sialic acid residues.
CC -!- DISEASE: Defects in TNFRSF11B are the cause of juvenile Paget
CC disease (JPD) (MIM:239000); also called hyperostosis corticalis
CC deformans juvenilis or hereditary hyperphosphatasia or chronic
CC congenital idiopathic hyperphosphatasia. JPD is a rare autosomal
CC recessive osteopathy that presents in infancy or early childhood.
CC The disorder is characterized by rapidly remodeling woven bone,
CC osteopenia, debilitating fractures, and deformities due to a
CC markedly accelerated rate of bone remodeling throughout the
CC skeleton. Approximately 40 cases of JPD have been reported
CC worldwide. Unless it is treated with drugs that block osteoclast-
CC mediated skeletal resorption, the disease can be fatal.
CC -!- SIMILARITY: Contains 2 death domains.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U94332; AAB53709.1; -;
CC EMBL: AB002146; BAA55910.1; -;
CC EMBL: AB008822; BAA32076.1; -;
CC EMBL: AB008821; BAA32076.1; JOINED.
CC EMBL: AY466112; AAR23265.1; -;
CC EMBL: BC030155; AAH30155.1; -;
CC EMBL: AF134187; AAF20168.1; -;
CC HSSP: O14763; IDOG.
CC Genew: HGNC:11909; TNFRSF11B.
CC MIM: 602643; -;
CC MIM: 239000; -;
CC GO: GO:0005576; C:extracellular; TAS.
CC GO: GO:0005125; F:cytokine activity; TAS.
CC GO: GO:0004872; F:receptor activity; TAS.
CC GO: GO:0007165; P:signal transduction; TAS.
CC GO: GO:0001501; P:skeletal development; TAS.
CC InterPro: IPR000488; Death.
CC InterPro: IPR011029; DEATH like.
CC InterPro: IPR009030; Growth_Fac_recept.
CC InterPro: IPR001368; TNFR_C5.

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DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SMO0005; DEATH; 1.

Query Match
Best Local Similarity 99.7%; Score 2079; DB 1; Length 401;
Matches 379; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQVKECNRTNHRVCEKGRYLEFCLKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 120
Db 82 YCSPVKELQVKECNRTNHRVCEKGRYLEFCLKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVTL 201

QY 181 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 261

QY 241 KAQDIVKKIIQDIDLCEVSVQRHGHANLTPFQRLSMLSESLPGKKVGAEDIEKTIKACKP 300
Db 262 KDQDIVKKIIQDIDLCEVSVQRHGHANLTPFQRLSMLSESLPGKKVGAEDIEKTIKACKP 321

QY 301 SDQILKLLSLWRIKNGQDYLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGQDYLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLFMIGNQVQSVKISL 380
Db 382 QKLFLFMIGNQVQSVKISL 401

RESULT 2
ID Q6PI12 PRELIMINARY; PRT; 401 AA.
AC Q6PI12;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
GN Name=tnfrsf11b;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

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Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RA Strausberg R.;
RA Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; AAH49782.1; -.
DR GO; GO:0005578; C:extracellular matrix; IDA.
DR GO; GO:0042489; P:negative regulation of ontogenesis (sensu. .; IDA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR Pfam; PF00020; TNFR_C6; 4-.
DR SMART; SMO0005; DEATH; 1.
DR SMART; SMO0208; TNFR; 4.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00020; TNFR_NGFR_2; 2.
DR PROSITE; PS00652; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 401 AA; 45965 MW; 7C708E52EB46BA0E CRC64;

Query Match
Best Local Similarity 88.0%; Score 1834; DB 2; Length 401;
Matches 329; Conservative 25; Mismatches 26; Indels 0; Gaps 0;

QY 1 ETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTVCAPCPDHYTDSWHTSDECL 60
Db 22 ETFPKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTVCAPCPDHYTDSWHTSDECL 81

QY 61 YCSPVKELQVKECNRTNHRVCEKGRYLEFCLKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 120
Db 82 YCSPVKELQVKECNRTNHRVCEKGRYLEFCLKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 141

QY 121 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVTL 180
Db 142 CKRCPDGFSSNETSSKAPCRKHTNCSVFGLLLTQKGNATHNICSGNSESTQKCGIDVTL 201

QY 181 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 240
Db 202 CEEAFFRFAVPTKFTPNWLSVLDNLPCTKVNABVERIKRQHSSEQOTFOLLKLWKHON 261

QY 241 KAQDIVKKIIQDIDLCEVSVQRHGHANLTPFQRLSMLSESLPGKKVGAEDIEKTIKACKP 300
Db 262 KDQDIVKKIIQDIDLCEVSVQRHGHANLTPFQRLSMLSESLPGKKVGAEDIEKTIKACKP 321

QY 301 SDQILKLLSLWRIKNGQDYLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 360
Db 322 SDQILKLLSLWRIKNGQDYLKGLMHALKHSKTYHFPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLFMIGNQVQSVKISL 380
Db 382 QKLFLFMIGNQVQSVKISL 401

RESULT 3
AAH49782
ID AAH49782 PRELIMINARY; PRT; 401 AA.
AC AAH49782;
DT 02-MAR-2004 (TrEMBLrel. 27, Created)
DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Tumor necrosis factor receptor superfamily, member 11b
DE (Osteoprotegerin).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Limb;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,
RA Fahy J., Helton E., Kettman M., Madan A.C., Rodriguez S., Gough G.G.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Rodriguez A.C., Grinchwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kzywinski M.I., Skalska U., Smalus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RA "Generation and initial analysis of more than 15,000 full-length human
RA and mouse cDNA sequences,"
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
PP SEQUENCE FROM N.A.
RC TISSUB=Limb;
RA Strausberg R.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC049782; AAH49782.1; -.
KW Receptor.
SQ SEQUENCE 401 AA; 45965 MW; 7C708B52EB46BA0E CRC64;

Query Match 88.0%; Score 1834; DB 2; Length 401;
Best Local Similarity 86.6%; Pred. No. 2.3e-122;
Matches 329; Conservative 25; Mismatches 26; Indels 0; Gaps 0;

QY 1 ETPFKYLYHDETSKAPCRKHTNCVGLLLTQGNATHNICGNSSESTQKCGIDVTL 60
DB 22 ETLPKYLYHDETSKAPCRKHTNCVGLLLTQGNATHNICGNSSESTQKCGIDVTL 60

QY 61 YGSPVCKELQVYQECNTHNRVCEKRGYLEIEFLKHSRCPGFGVQAGTPEINIV 120
DB 82 YGSPVCKELQVYQECNTHNRVCEKRGYLEIEFLKHSRCPGFGVQAGTPEINIV 141

QY 121 CKRCPDGFNSSTKAPCRKHTNCVGLLLTQGNATHNICGNSSESTQKCGIDVTL 180
DB 142 CKKCPDGFNSSTKAPCRKHTNCVGLLLTQGNATHNICGNSSESTQKCGIDVTL 201

QY 181 CEAEFFRAVPKFTPNMVLVDNLPGTKVAESVERIKRHSOEOFTQKLLWKQCN 240
DB 202 CEAEFFRAVPKFTPNMVLVDNLPGTKVAESVERIKRHSOEOFTQKLLWKQCN 261

QY 241 KAQDITVKKIIDIICENSQVRHIGHANLTFFQLRSLMESLPKGVGADIEKTIKACP 300
DB 262 RQENVKVKIIDIICENSQVRHIGHANLTFFQLRSLMESLPKGVGADIEKTIKACP 321

QY 301 SQIILKLSLWIKNGQDTLKGMLHAKHSKTYHPPKTVTQSLKKTIRFLHSFTMYKLY 360
DB 322 SEQLLKLSLWIKNGQDTLKGMLHAKHSKTYHPPKTVTQSLKKTIRFLHSFTMYKLY 381

QY 361 QKLFLEMIGNQVSKISCL 380
DB 382 QKLFLEMIGNQVSKISCL 401

RESULT 4
ID T11B RAT
AC 008727; STANDARD; PRT; 401 AA.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin).
GN Name=Tnfrsf1b; Synonyms=Opg;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
TISSUB=Embryonic intestine;
MEDLINE=97262071; PubMed=9108485;
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
RA Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
RA Suggs S., Boyle W.J.,
RA "Osteoprotegerin: a novel secreted protein involved in the regulation
RA of bone density,"
RA Cell 89:309-319 (1997).
RL CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis. Bone homeostasis
CC seems to depend on the local RANKL/OPG ratio. May also play a role
CC in preventing arterial calcification. May act as decoy receptor
CC for TRAIL and protect against apoptosis. TRAIL binding blocks the
CC inhibition of osteoclastogenesis (By similarity).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- INDUCTION: Up-regulated by osteopontin.
CC -!- SIMILARITY: Contains 2 death domains.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC
CC EMBL; U94330; AAB53707.1; -.
CC HSP; P19438; INCF.
CC RGD; 619802; Tnfrsf1b.
CC InterPro; IPR00488; Death.
CC InterPro; IPR011029; DEATH like.
CC InterPro; IPR009030; Growth_fac_recept.
CC InterPro; IPR001368; TNFR_c6.
CC Pfam; PF00020; TNFR_c6; 4.
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00117; DEATH_DOMAIN; FALSE_NEG.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00505; TNFR_NGFR_2; 2.
CC Apoptosis; Cytokine; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21 By similarity.
FT CHAIN 22 401 Tumor necrosis factor receptor
FT superfamily member 11B.
FT REPEAT 24 62 TNFR-Cys 1.
FT REPEAT 65 105 TNFR-Cys 2.
FT REPEAT 107 142 TNFR-Cys 3.
FT REPEAT 145 185 TNFR-Cys 4.
FT DOMAIN 198 269 Death 1.
FT DOMAIN 270 365 Death 2.
FT SITE 400 400 Involved in dimerization (By similarity).
FT DISULFID 41 54 By similarity.
FT DISULFID 44 62 By similarity.
FT DISULFID 65 80 By similarity.
FT DISULFID 83 97 By similarity.
FT DISULFID 87 105 By similarity.
FT DISULFID 107 118 By similarity.
FT DISULFID 124 142 By similarity.
FT DISULFID 145 160 By similarity.
FT DISULFID 166 185 By similarity.
FT CARBOHYD 98 98 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 165 165 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 178 178 N-linked (GlcNAc...) (Potential).
FT CARBOHYD 289 289 N-linked (GlcNAc...) (Potential).
FT SEQUENCE 401 AA; 46192 MW; FEC6A31F1D4E573A CRC64;


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FT DISULFID 87 105 By similarity.
FT DISULFID 107 118 By similarity.
FT DISULFID 124 142 By similarity.
FT DISULFID 145 160 By similarity.
FT DISULFID 166 185 By similarity.
FT CARBOHYD 98 105 N-linked (GlcNAc...) (potential).
FT CARBOHYD 165 178 N-linked (GlcNAc...) (potential).
FT CARBOHYD 178 185 N-linked (GlcNAc...) (potential).
FT CARBOHYD 289 296 N-linked (GlcNAc...) (potential).
FT VARIANT 138 138 R -> P (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 161 161 I -> R (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 165 165 N -> D (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 288 288 S -> A (in strain 129/Ola and strain NIH Swiss).
FT VARIANT 296 296 L -> R (in strain 129/Ola and strain NIH Swiss).
SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;

Query Match 87.3%; Score 1820; DB 1; Length 401;
Best Local Similarity 86.1%; Pred. No. 2.3e-121;
Matches 327; Conservative 25; Mismatches 28; Indels 0; Gaps 0;

QY 1 ETEPPKYLHYDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDECL 60
DB 22 ETLPPKYLHYDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDECV 81

QY 61 YCSPVKELQVYKQECNTHNRVCECKEGRYLEIFFCFLKHSRSCPPGFGVQAGTPERNIV 120
DB 82 YCSPVKELQVYKQECNTHNRVCECKEGRYLEIFFCFLKHSRSCPPGFGVQAGTPERNIV 141

QY 121 CKRCPDGFPSNETSSKAPCRKHTNCSVGLLLTQGNATHNICSNGSESTOKCGIDVTIL 180
DB 142 CKKCPDGFPSNETSSKAPCRKHTNCSVGLLLTQGNATHNICSNGSESTOKCGIDVTIL 201

QY 181 CEEAFRAVPTKFTPNMLSVLDNLPGTKVNAESVERIKRQHSSEQEQTQFLLKLWKHQN 240
DB 202 CEEAFRAVPTKFTPNMLSVLDNLPGTKVNAESVERIKRQHSSEQEQTQFLLKLWKHQN 261

QY 241 KAQDIVKKIQQIDILCENSQVORHIGHANLTFQLSLMESLPKGVKVGADIEKTKACKP 300
DB 262 RQEMVKKIQQIDILCENSQVORHIGHANLTFQLSLMESLPKGVKVGADIEKTKACKP 321

QY 301 SDQILKLSLWRIKNGDQDTLKGMLHAKHSKTYHPPKTVTOSLAKTIRFLHSFTWKLYI 360
DB 322 SEQLLKLSLWRIKNGDQDTLKGMLHAKHSKTYHPPKTVTOSLAKTIRFLHSFTWKLYI 381

QY 361 QKLFLEMIGNOVQSVKISCL 380
DB 382 QKLFLEMIGNOVQSVKISCL 401

RESULT 6
Q6GLN3
ID Q6GLN3 PRELIMINARY; PRT; 387 AA.
AC Q6GLN3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

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RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Boraldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.B., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RL initiative.";
RN Dev. Dyn. 225:384-391(2002).
[3]
RP SEQUENCE FROM N.A.
RC TISSUE=Eye;
RA Klein S., Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; BC074428; AAH74428.1; -.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Hypothetical protein.
SQ SEQUENCE 387 AA; 44568 MW; F365C364A11484AA CRC64;

Query Match 49.3%; Score 1028.5; DB 2; Length 387;
Best Local Similarity 48.7%; Pred. No. 4.7e-65;
Matches 182; Conservative 68; Mismatches 111; Indels 13; Gaps 5;

QY 4 PKYLYHDEETSHQLLCKCPGTYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDECLYCS 63
DB 24 PKYSHYDPTSMYLCQDCHCPGTYLKQHTAKWKTVCAPCPDHYVYDTSWHTSDECLYCS 83

QY 64 PVCKELQVYKQECNTHNRVCECKEGRYLEIFFCFLKHSRSCPPGFGVQAGTPERNIVCKR 123
DB 84 VVCKELQVYKQECNTHNRVCECKEGRYLEIFFCFLKHSRSCPPGFGVQAGTPESDTCRP 143

QY 124 CPDGFPSNETSSKAPCRKHTNCSVGLLLTQGNATHNICSNGSESTOKCGIDVTLCBE 183
DB 144 CPEGTFSDSTATARCQKHTDCKKLGIVKAYQSDSDHDTLCQPEGSF---CEIDITLCE 200

QY 184 AFREFAVPTKFTPNMLSVLDNLPGTKVNAESVERIKRQHSSEQEQTQFLLKLWKHQNKAQ 243
DB 201 AFREFAVPTKFTPNMLSVLDNLPGTKVNAESVERIKRQHSSEQEQTQFLLKLWKHQNKAQ 255

QY 244 DIVKKIQQIDILCENSQVORHIGHANLTFQLSLMESLPKGVKVGADIEKTKACKPSPQ 303
DB 256 ESGKHLFDQLQVCEKVKVSKHIGKLNVTATQLATLAKSLFGNKISKRELETTVKICSPDQ 315

QY 304 ILKLSLWRIKNGDQDTLKGMLHAKHSKTYHPPKTVTOSLAKTIRFLHSFTWKLYOKL 363
DB 316 VLKLSLWRIKNGDQDTLKGMLHAKHSKTYHPPKTVTOSLAKTIRFLHSFTWKLYOKL 370

QY 364 FLEMIGNOVQSVK 377

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Db 371 LLEIFGSGTQPAKV 384

RESULT 7
Q7ZZY4 PRELIMINARY; PRT; 146 AA.
AC Q7ZZY4;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Osteoprotegerin (Fragment).
GN Name=OPG;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22760275; PubMed=12878204;
RA Bridgman J.T., Johnson A.L.;
RT "Characterization of chicken TNFR superfamily decoy receptors, DcR3
and osteoprotegerin."; Commun. 307:956-961(2003).
RL Biochem. Biophys. Res. Commun. 307:956-961(2003).
DR EMBL; AY251407; AAP03890.1; -.
GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
FT NON TER 146
SQ SEQUENCE 146 AA; 16487 MW; 1C9E64FE3A0FC2DF CRC64;

Query Match 25.2%; Score 525; DB 2; Length 146;
Best Local Similarity 69.7%; Pred. No. 1e-29;
Matches 85; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 4 PPXYLYHDETSQLLCDKCPGPGTYLKQHTAKWTVCAKCPDHYTDSWHTSDECLYCS 63
Db 25 PPXYLYHDETSQVNCNQCPCPGSYVKQHTAASPTVCAPCPDQYVAEDWNSNDEQYCS 84
QY 64 PVCKELQYVQKQECNRTHNRVCEKGEGRYLEIFCLKHSRCPGPGVYVQAGTPERNTVCKR 123
Db 85 AVCKELQYIKQRTSTQDRVCEICIEGWYLEIFCLKHTCPCPGVQAQGPSPSDTVCF 144
QY 124 CP 125
Db 145 CP 146

RESULT 8
Q7ZZY5 PRELIMINARY; PRT; 186 AA.
AC Q7ZZY5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Decoy receptor 3 (Fragment).
GN Name=DcR3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22760275; PubMed=12878204;
RA Bridgman J.T., Johnson A.L.;
RT "Characterization of chicken TNFR superfamily decoy receptors, DcR3

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RT and osteoprotegerin.";
RL Biochem. Biophys. Res. Commun. 307:956-961(2003).
DR EMBL; AY251406; AAP03889.1; -.
GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac_recept.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
FT NON TER 186
SQ SEQUENCE 186 AA; 20671 MW; 31D65731DACB758E CRC64;

Query Match 21.6%; Score 450; DB 2; Length 186;
Best Local Similarity 48.7%; Pred. No. 3e-24;
Matches 75; Conservative 24; Mismatches 55; Indels 0; Gaps 0;

QY 4 PPXYLYHDETSQLLCDKCPGPGTYLKQHTAKWTVCAKCPDHYTDSWHTSDECLYCS 63
Db 32 PPTYQWRDAGTKERVTCQQCPGPGTFVAQHCTKERTVTCAPCPDLHYTHYNNYLEKCLYCN 91
QY 64 PVCKELQYVQKQECNRTHNRVCEKGEGRYLEIFCLKHSRCPGPGVYVQAGTPERNTVCKR 123
Db 92 VXGGERVQVQCNATHNRACQCEGHAEMEFVQHSEXXPGSGVVKLGSPSENTQCR 151
QY 124 CPDGFESNETSSKAPCRKKTNCVSFGLLLTKGN 157
Db 152 CPRGFSFSSSSSTPCRAHQNCQLGKENTVPGN 185

RESULT 9
TR6B HUMAN STANDARD; PRT; 300 AA.
AC O95407;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 6B precursor (Decoy
receptor for Fas ligand) (Decoy receptor 3) (DcR3) (M68)
DE (UNQ186/PRO12).
DE Name=TNFRSF6B; Synonyms=DcR3, TR6;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal lung;
RX MEDLINE=99087326; PubMed=9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.
RC TISSUE=Prostate;
RX MEDLINE=99253915; PubMed=1018773;
RA Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGM-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=20122600; PubMed=10655513;
RA Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;

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RT	"Overexpression of M68/DeB3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster."
RT	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235 (2000).
RT	[4]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=22897296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi L., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wian D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.L., Godowski P., Gray A.;
RA	"The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a bioinformatics assessment";
RT	Genome Res. 13:2265-2270 (2003).
RT	[5]
RP	SEQUENCE FROM N.A.
RP	MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA	Deloukas P., Matthews L.H., Ashurst J.L., Burton J., Gilbert J.G.R., Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L., Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M., Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J., Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P., Clee C.M., Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clegg S., Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M., Ellington A.G., Frankland J.A., Fraser A., French L., Garner P., Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E., Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J., Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D., Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S., Leharvalho M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D., Marsh V.L., Martin S.L., McConachie L.J., McClay K., McMurray A.A., Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T., Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I., Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H., Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkneen R., Sims S., Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E., Swann R.M., Symamore N., Vaudin M., Wall M., Wallis J.M., Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S.A., Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S., Rogers J.;
RT	"The DNA sequence and comparative analysis of human chromosome 20.";
RL	Nature 414:865-871 (2001).
RT	[6]
RP	SEQUENCE FROM N.A.
RP	TISSUE=Lung, and Skin;
RC	MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L., Stappleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Rosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
RT	

RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
CC	-1- FUNCTION: Decoy receptor for the cytotoxic ligands TNFSF14/LIGHT and TNFSF6/PASL. Protects against apoptosis.
CC	-1- SUBCELLULAR LOCATION: Secreted.
CC	-1- TISSUE SPECIFICITY: Detected in fetal lung, brain and liver.
CC	Detected in adult stomach, spinal cord, lymph node, trachea, spleen, colon and lung. Highly expressed in several primary tumors from colon, stomach, rectum, esophagus and in SW480 colon carcinoma cells.
CC	-1- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	EMBL; AF104419; AAD03056.1; -
DR	EMBL; AF134240; AAD29688.1; -
DR	EMBL; AF217796; AAF35244.1; -
DR	EMBL; AF217793; AAF33685.1; -
DR	EMBL; AF217794; AAF33686.1; -
DR	EMBL; AY358279; AAQ88646.1; -
DR	EMBL; AL121845; CAC03668.1; -
DR	EMBL; BC017065; AAH17065.1; -
DR	EMBL; BC034349; AAH34349.1; -
DR	HSSP; O14763; 1DU3.
DR	Genew; HGNC:11921; TNFRSF6B.
DR	MIM; 603361; -
DR	GO; GO:0005625; C:soluble fraction; TAS.
DR	GO; GO:0004872; F:receptor activity; TAS.
DR	GO; GO:0006916; P:anti-apoptosis; TAS.
DR	InterPro; IPR009030; Grow fac_recept.
DR	InterPro; IPR001368; TNFR_C6.
DR	Pfam; PF00020; TNFR_C6; 4.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS00652; TNFR_NGFR 1; 1.
DR	PROSITE; PS00500; TNFR_NGFR 2; 2.
KW	Apoptosis; Direct protein sequencing; Glycoprotein; Receptor; Repeat; Signal.
FT	CHAIN 1 29
FT	SIGNAL 30 300
FT	REPEAT 31 70 Tumor necrosis factor receptor
FT	REPEAT 72 113 superfamily member 6B.
FT	REPEAT 115 150 TNFR-Cys 1.
FT	REPEAT 152 193 TNFR-Cys 2.
FT	REPEAT 152 193 TNFR-Cys 3.
FT	DISULFID 49 62 TNFR-Cys 4.
FT	DISULFID 52 70 By similarity.
FT	DISULFID 73 88 By similarity.
FT	DISULFID 91 105 By similarity.
FT	DISULFID 95 113 By similarity.
FT	DISULFID 115 126 By similarity.
FT	DISULFID 132 150 By similarity.
FT	DISULFID 153 168 By similarity.
FT	DISULFID 174 193 By similarity.
FT	CARBOHYD 173 173 N-linked (GlcNAc...) (Potential).
SQ	SEQUENCE 300 AA; 32679 MW; F90AEB3718449AF CRC64;
	Query Match 21.1%; Score 440.5; DB 1; Length 300;
	Best Local Similarity 41.2%; Pred. No. 2.5e-23;
	Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
QY	5 PKYLHVDTEHSLLCDKCPGTYLKHCTAKWTKVCAPCPHYYTDSWHTSDECLYCSP 64
DB	34 PTPWRDAETGERLVCAQCPPTGTVQVPCRRSPITCGPCPRHYTFQWYLERCRYCNV 93
QY	65 VKELQYVKQECNRTNHRVCECKEGRYLIEFCLKHSRCPGPGVQAGTPERTVCKRC 124
DB	94 LCGEREERARACHATHNACRCKRTGFFAHAGFCLHASCPPGAGVIAPGTPTSQCCPC 153

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QY 125 PDGFFNETSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNBESTQKCGIDVTLG 181
Db 154 PPGTFSSASSSEQCPHRNCTALGALNVPSSSHDLTCTGTFPLSTRVPGAER--C 211

QY 182 EBAFFRF 198
Db 212 ERAVIDF 218

RESULT 10
Q9PUS0 PRELIMINARY; PRT; 302 AA.
AC Q9PUS0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Decoy TNF receptor.
OS Salvelinus fontinalis (Brook trout) (Brook char).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
NCBI_TaxID=8038;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20111091; PubMed=10642582;
RA Bobe J., Goetz F.W.;
RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
RT the brook trout (Salvelinus fontinalis) ovary at the completion of
RT ovulation."
RL Biol. Reprod. 62:420-426(2000).
DR EMBL; AF156738; AAD56428.1; -.
DR HSSP; O14763; 1D4V.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000208; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MW; E44C73477F05C3DF CRC64;

Query Match 19.7%; Score 411.5; DB 2; Length 302;
Best Local Similarity 32.0%; Pred. No. 2.9e-21;
Matches 96; Conservative 57; Mismatches 110; Indels 37; Gaps 9;

QY 11 DRETSQLLCDKCPPTLYLKQHCCTAKWTVCAPCPDHYHYDTSWHTSDECLYSPVCKELQ 70
Db 27 DRYSGLSIVCDRCPPGTYLRAPCSAMRKSDCAPCPNGAYTEFWNHLSKLRCS-MCAENQ 85

QY 71 YVQECNRTNHRVCECKEGRYL--EIEFCLKHSRCPGFGVQAGTPERTVCKRCPDGF 128
Db 86 VVQKCSPPNCECECKEGYFNKYACIKKECPGPGANTGPHQDTECVQCAQF 145

QY 129 FNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNICSGNSESTQKCGIDVTLCEEAFFRF 188
Db 146 YSEVSSAKATCLAQSNCKVGLRVLLKGDWENTLASCVDLKTGDAE-----YLHE 198

QY 189 AVPTKFTPNWLSVLDNLEGTKNVRESVERIKRQHSSEQTQLLKLWQKHAQDIVKK 248
Db 199 ILPTFF-----QLHQTMGIRMRRLAMRLPQEGGKPLIGAVMK--RNRRLGHDFM-- 248

QY 249 ITQIDILCNSVQRHGHANLTFEQLRSIMESI;PGKKVGAEDI-EKTIKACKPSDILKL 307
Db 249 -----NSWDQAGN-----DQVKLPEVL--RKIGAFNMGDKLERKLAIDQQSKL 292

RESULT 11
Q90W71 PRELIMINARY; PRT; 285 AA.
AC Q90W71;
DT 01-DEC-2001 (Tremblrel. 19, Created)

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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Putative decoy receptor 3 protein.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Head kidney;
RA Pleguezuelos O., Secombes C.J.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ315137; CAC43329.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR009030; Grow fac recept.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF000208; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 285 AA; 31642 MW; F575CFFC1E391AD0 CRC64;

Query Match 18.2%; Score 380.5; DB 2; Length 285;
Best Local Similarity 38.1%; Pred. No. 4.3e-19;
Matches 74; Conservative 25; Mismatches 88; Indels 7; Gaps 3;

QY 5 PKYLHYDETSQLLCDKCPPTLYLKQHCCTAKWTVCAPCPDHYHYDTSWHTSDECLYSP 64
Db 29 PTYWRDDATGSLTCDLCAPGTYLLKHCTDKRSCDCGCPKSHYTEIMWYIERCQYCNR 88

QY 65 VKELQVYQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVQAGTPERTVCKRC 124
Db 89 FCTADIESVPTQLNHRQCECKDGFYTHGSCSRHRRCPGEGVISNGTAHTDVKCEPC 148

QY 125 PDGFFNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI-CSG--NSESTQKCGIDVTLCE 182
Db 149 PVGFFSAVSSRRKACQKFSVCPGG--TTIPGNDMDVYCSACTNGSRTHE---GEAICD 203

QY 183 EAFFRAVPTKTP 196
Db 204 GELMEFLSLQILTP 217

RESULT 12
Q90YS6 PRELIMINARY; PRT; 285 AA.
AC Q90YS6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE TNF decoy receptor.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
NCBI_TaxID=8022;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21883732; PubMed=11886174;
RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
RT fragments containing AU-rich elements."
RL Cytokine 17:71-81(2002).
DR EMBL; AF401631; AAK91758.1; -.
DR HSSP; O14763; 1D0G.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR006209; EGF like.

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DR	InterPro; IPR009030; Grow fac_recept.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 3.
DR	SMART; SM00208; TNFR; 3.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS00050; TNFR_NGFR_2; 1.
KW	Receptor.
SQ	SEQUENCE 285 AA; 31795 MW; 5E3BD1B6FC6BABC CRC64;
	Query Match 17.9%; Score 372.5; DB 2; Length 285;
	Best Local Similarity 37.6%; Pred. No. 1.6e-18;
	Matches 73; Conservative 25; Mismatches 89; Indels 7; Gaps 3;
Qy	5 PKYLHYDEETSHOLLCDKCPGGYLYKHCTAKWKTVCAPCDPDHYVDTSDWHSTDECLYCSP 64
Dd	29 PTIWRDDATGDSLTCDLCAPIGLLHKTKRKSCDCGPCSKSHYTEIWNYYIERQYCNR 88
Qy	65 VCKELQVVQECNRTNRNVCECKEGRYLETFCLFKHRSPPGVVGVOAGTPERTNTVKRC 124
Dd	89 FCTADEIESVPCTQLHNROCECKDFMYTHGSCSRHRRCPPGEVLSNGTAHTDVKCEPC 148
Qy	125 PDGFFSNETSSKAPCRKHTNCVSFGLLLTQKGNAHDNICSG--NSRSTQKCGIDVTICE 182
Dd	149 PVGFFSAVSSRRACQFSYCPPG--RTTIIPGNMNDVVCASCRNGSRTHE---GOAICD 203
Qy	183 EAFFRAVPTKFTP 196
Dd	204 GELMEFLSLQLITP 217
RESULT 13	
Q6NW61	PRELIMINARY; PRT; 286 AA.
AC	Q6NW61
DT	05-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DN	LOC407674 protein (Fragment).
GN	Name=LOC407674;
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.E.,
RA	Jones S.J., Marra M.A.;
RT	"Generation and initial analysis of more than 15,000 full-length human
RL	and mouse cDNA sequences";
RN	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RA	Strausberg R.;

RL	Submitted (MAR-2004) to the EMBL/GenBank/DDJB databases.
DR	EMBL; BC067712; AAH67712.1; --
DR	InterPro; IPR001368; TNFR_c6.
DR	InterPro; IPR001368; EGF like.
DR	InterPro; IPR001368; TNFR_c6.
DR	Pfam; PF00020; TNFR_c6; 4.
DR	SMART; SM00208; TNFR; 4.
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR	PROSITE; PS00050; TNFR_NGFR_2; 1.
ET	NON TER 1
SQ	SEQUENCE 286 AA; 32275 MW; 9F43CDC5FAC4E77B CRC64;
	Query Match 17.5%; Score 365; DB 2; Length 286;
	Best Local Similarity 32.4%; Pred. No. 5.5e-18;
	Matches 89; Conservative 41; Mismatches 119; Indels 26; Gaps 6;
Qy	7 YLHYDEETSQLLCDKCPGTLYKHCTAKWKTVCAPCDPDHYVDTSDWHSTDECLYCSPVC 66
Dd	18 YRKADPETGTLTECARCAPGSRLRQCSSSRQTCSFGCGXYTFWFNYIPDCLLCDS-C 76
Qy	67 KELQYVKEQNRTNRNVCECKEGRYLEIFCLFKHRSPPGVVGVOAGTPERTNTVKRCPD 126
Dd	77 AEHQRVVQPCNGLIANTVCECEGFGYWEQHFCHRHVSVCRFCHGYKTAGTYSVTVCBAE 136
Qy	127 GFPSNETSSKAPCRKHTNCVSFGLLLTQKGNAHDNICSGNSESTQKCGIDVTLCHEAF 186
Dd	137 GHFSDATKAHAQCCKVRVCOGBEHLLL-SGNTHINSICTCCOOLSNNGWVTAIVEDPAL 195
Qy	187 RFAVPTKFTENWLVLVDNLPGTKVNAESVERIKQHSSQEOTFQLKLKMKH-ONKAQDI 245
Dd	196 ALQVOOKIDIHRLQMV-----IRRLKK-----PLKQLHKGTAMRADP 234
Qy	246 VKTIQIDILCENSQVORHGHANLTPEOLRLSMES 280
Dd	235 SEGILDRSMMLSESYLSHL--AQRMQTNIARRVQOS 267
RESULT 14	
AAH67712	PRELIMINARY; PRT; 286 AA.
ID	AAH67712
AC	AAH67712;
DT	24-MAY-2004 (TrEMBLrel. 27, Created)
DT	24-MAY-2004 (TrEMBLrel. 27, Last sequence update)
DT	24-MAY-2004 (TrEMBLrel. 27, Last annotation update)
DE	LOC407674 protein (Fragment).
GN	LOC407674.
OS	Brachydanio rerio (Zebrafish) (Danio rerio).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC	Cyprinidae; Danio.
OX	NCBI_TaxID=7955;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Embryo;
RX	MEDLINE=22388257; PubMed=12477932;
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA	Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA	Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA	Fahay J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA	

